



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 100503

TO: Konstantina Katcheves
Location: CM1/11C01/11E12 /
Art Unit: 1636
Friday, August 08, 2003

Case Serial Number: 09/846797

From: Mona Smith
Location: Biotech-Chem Library
CM1-6A01
Phone: 308-3278

mona.smith@uspto.gov

Search Notes

See attached results.

Thank you for using STIC services
Feel free to contact me if you have any questions.

Mona Smith
308-3278

180 523

STIC-Biotech/ChemLib

RECEIVED

AUG-5 2003

(STIC)

From: Fredman, Jeffrey
Sent: Tuesday, August 05, 2003 11:24 AM
To: STIC-Biotech/ChemLib
Cc: Katcheves, Konstantina
Subject: FW: RUSH sequence search 09/846797
 PLEASE RUSH.

I Approve.

Jeff Fredman

-----Original Message-----

From: Katcheves, Konstantina
Sent: Monday, August 04, 2003 3:26 PM
To: Fredman, Jeffrey
Subject: RUSH sequence search 09/846797

Application serial number: 09/846797

Please search SEQ ID NOs:1 and 6 against the commercial databases only. (29 na and 35 na respectively)

Thank you,
 Tina

Konstantina Katcheves
Art Unit 1636
Phone: 305-1999
Office: 11B15
Mailbox: 11E12

M, SM, TN

21A

8/5/03

8/8/03

3
5
5

8/5/03

Katcheves, Konstantina

Fr m: Fredman, Jeffrey
S nt: Tuesday, August 05, 2003 11:24 AM
To: STIC-Biotech/ChemLib
Cc: Katcheves, Konstantina
Subject: FW: RUSH sequence search 09/846797

PLEASE RUSH.

I Approve.

Jeff Fredman

-----Original Message-----

From: Katcheves, Konstantina
Sent: Monday, August 04, 2003 3:26 PM
T : Fredman, Jeffrey
Subject: RUSH sequence search 09/846797

Application serial number: 09/846797

Please search SEQ ID NOs:1 and 6 against the commercial databases only. (29 na and 35 na respectively)

Thank you,
Tina

Konstantina Katcheves
Art Unit 1636
Phone: 305-1999
Office: 11B15
Mailbox: 11E12

Katcheves, Konstantina

To: Fredman, Jeffrey

Subject: RUSH sequence search 09/846797

2/1/03

Application serial number: 09/846797

Please search SEQ ID NOs:1 and 6 against the commercial databases only. (29 na and 35 na respectively)

Thank you,
Tina

Konstantina Katcheves

Art Unit 1636

Phone: 305-1999

Office: 11B15

Mailbox: 11E12

8/4/03

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 6, 2003, 22:51:21 : Search time 1893.28 Seconds
(without alignments)
449.303 Million cell updates/sec

Title: US-09-846-797-6
Perfect score: 35
Sequence: 1 ctatgcgcataagttatggttaagactacacg 35

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_iny:*
19: em_gss_pln:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vtl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	100.0	157	12	BM870744
2	100.0	163	9	AU007416
3	100.0	177	9	AU010787
4	100.0	184	9	AU010656

Result No.	Score	Query Match length	ID	Description
5	100.0	184	9	AU010788
6	100.0	184	9	AU010834
7	100.0	184	9	AU010835
8	100.0	184	9	AU010835
9	100.0	184	9	AU010835
10	100.0	184	9	AU010835
11	100.0	184	9	AU010835
12	100.0	184	9	AU010835
13	100.0	184	9	AU010835
14	100.0	184	9	AU010835
15	100.0	184	9	AU010835
16	100.0	184	9	AU010835
17	100.0	184	9	AU010835
18	100.0	184	9	AU010835
19	100.0	184	9	AU010835
20	100.0	184	9	AU010835
21	100.0	184	9	AU010835
22	100.0	184	9	AU010835
23	100.0	184	9	AU010835
24	100.0	184	9	AU010835
25	100.0	184	9	AU010835
26	100.0	184	9	AU010835
27	100.0	184	9	AU010835
28	100.0	184	9	AU010835
29	100.0	184	9	AU010835
30	100.0	184	9	AU010835
31	100.0	184	9	AU010835
32	100.0	184	9	AU010835
33	100.0	184	9	AU010835
34	100.0	184	9	AU010835
35	100.0	184	9	AU010835
36	100.0	184	9	AU010835
37	100.0	184	9	AU010835
38	100.0	184	9	AU010835
39	100.0	184	9	AU010835
40	100.0	184	9	AU010835
41	100.0	184	9	AU010835
42	100.0	184	9	AU010835
43	100.0	184	9	AU010835
44	100.0	184	9	AU010835
45	100.0	184	9	AU010835

ALIGNMENTS

RESULT 1
LOCUS BM870744/c
DEFINITION mgnso11xm14f.b Magnaporthe grisea NS Uni-Zap XR Library Magnaporthe
ACCESSION BM870744
VERSION BM870744.2 GI:30404361
KEYWORDS EST.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes Incertae sedis; Magnaportheaceae; Magnaporthe.
AUTHORS Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai
K. and Dean,R.A.
TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe
grisea
JOURNAL Unpublished
COMMENT On Mar 7, 2002 this sequence version replaced gi:19338426.
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact person

Best nr hit (April. 22, 2003) ref1NF_701347.1| hypothetical protein [plasmodium falciparum 3D7]... 44 5e-04

PCR primers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgns011 row: M column: 14
Seq primer: T3.

FEATURES

Location/Qualifiers
1..157
/organism="Magnetorthe grisea"
/mol_type="mRNA"
/strain="Guy11"
/db_xref="taxon:148305"
/clone="mgns011xm14"
/sex="Mali-2 hermaphrodite"
/cell_type="mycelium"
/clone_lib="Magnetorthe grisea NS Uni-Zap XR Library"
/note="vector: pBluescriptSK-; Site_1: EcoRI; Site_2: XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Nitrogen starvation library. Cells were inoculated into minimal medium and grown for two days with shaking (150 rpm) at room temperature. Culture was harvested, blended, inoculated into minimal medium as above for 24 h. Cells were harvested, washed with water and inoculated into minimal medium base lacking nitrogen source for 6 h. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

BASE COUNT
44 a 31 c 39 g 43 t

ORIGIN

Query Match 100.0%; Score 35; DB 12; Length 157;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGTCGGCATAGTTATGTTAGACTACGACG 35
|||||
93 CTAGTCGGCATAGTTATGTTAGACTACGACG 59

RESULT 2

AU007416

LOCUS 163 bp mRNA linear EST 31-JUL-1998
DEFINITION AU007416 Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe cDNA clone spc01943, mRNA sequence.

ACCESSION AU007416
VERSION AU007416.1 GI:3343874

KEYWORDS EST
Schizosaccharomyces pombe (fission yeast)
Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.

REFERENCE 1 (bases 1 to 163)
Moriyomo, M. and Mita, K.
Identification of expressed sequence tags of Schizosaccharomyces pombe

JOURNAL Unpublished
COMMENT Contact: Mitsuoki Moriyomo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, 263-8555, Japan
Email: moriyomo@nirs.go.jp.

FEATURES

Location/Qualifiers
1..163
/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/strain="972"
/db_xref="taxon:4896"

/clone="spc01943"
/sex="h minus"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/note="vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, <http://www.nirs.go.jp>)"

BASE COUNT
46 a 37 c 33 g 47 t

ORIGIN

Query Match 100.0%; Score 35; DB 9; Length 163;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGTCGGCATAGTTATGTTAGACTACGACG 35
|||||
68 CTAGTCGGCATAGTTATGTTAGACTACGACG 102

RESULT 3

AU010787

LOCUS 177 bp mRNA linear EST 31-JUL-1998
DEFINITION AU010787 Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe cDNA clone spc10371, mRNA sequence.

ACCESSION AU010787
VERSION AU010787.1 GI:3347467
KEYWORDS EST
Schizosaccharomyces pombe (fission yeast)
Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.

REFERENCE 1 (bases 1 to 177)
Moriyomo, M. and Mita, K.
Identification of expressed sequence tags of Schizosaccharomyces pombe

JOURNAL Unpublished
COMMENT Contact: Mitsuoki Moriyomo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, 263-8555, Japan
Email: moriyomo@nirs.go.jp.

FEATURES

Location/Qualifiers

1..177
/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/strain="972"
/db_xref="taxon:4896"
/clone="spc10371"
/sex="h minus"

/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/note="vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, <http://www.nirs.go.jp>)"

BASE COUNT
46 a 38 c 34 g 55 t

ORIGIN

Query Match 100.0%; Score 35; DB 9; Length 177;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGTCGGCATAGTTATGTTAGACTACGACG 35
|||||
61 CTAGTCGGCATAGTTATGTTAGACTACGACG 95

RESULT 4

AU010656

LOCUS AU010656 184 bp mRNA linear EST 31-JUL-1998
 DEFINITION AU010656 Schizosaccharomyces pombe late log phase cDNA
 Schizosaccharomyces pombe spc10200, mRNA sequence.
 ACCESSION AU010656
 VERSION AU010656.1 GI:3347336
 KEYWORDS EST
 SOURCE Schizosaccharomyces pombe (fission yeast)
 ORGANISM Schizosaccharomyces pombe
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 Schizosaccharomycetales; Schizosaccharomycetaceae;
 Schizosaccharomyces.
 REFERENCE 1 (bases 1 to 184)
 AUTHORS Moriyono,M. and Mita,K.
 TITLE Identification of expressed sequence tags of Schizosaccharomyces pombe

JOURNAL
 COMMENT Unpublished
 Contact: Mitsunori Moriyono
 Genome Research Group
 National Institute of Radiological Sciences
 9-1, Anagawa-4-chome, Inage-Ku, Chiba 263-8555, Japan
 Email: moriyono@nirs.go.jp.
 Location/Qualifiers
 1.184
 /organism="Schizosaccharomyces pombe"
 /mol_type="mRNA"
 /strain="972"
 /db_xref="taxon:4896"
 /clone="spc10200"
 /sex="h minus"
 /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
 /note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"

BASE COUNT 48 a 42 c 38 g 56 t

ORIGIN

Query Match 100.0%; Score 35; DB 9; Length 184;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CTAGTCGCATAGTTATGTTAGTACGACG 35
 |||||
 68 CTAGTCGCATAGTTATGTTAGTACGACG 102

Qy

RESULT 5
 AU010788 184 bp mRNA linear EST 31-JUL-1998
 LOCUS AU010788 Schizosaccharomyces pombe late log phase cDNA
 Schizosaccharomyces pombe cDNA clone spc10372, mRNA sequence.
 ACCESSION AU010788
 VERSION AU010788.1 GI:3347468
 KEYWORDS EST
 SOURCE Schizosaccharomyces pombe (fission yeast)
 ORGANISM Schizosaccharomyces pombe
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 Schizosaccharomycetales; Schizosaccharomycetaceae;
 Schizosaccharomyces.
 REFERENCE 1 (bases 1 to 184)
 AUTHORS Moriyono,M. and Mita,K.
 TITLE Identification of expressed sequence tags of Schizosaccharomyces pombe

JOURNAL
 COMMENT Unpublished
 Contact: Mitsunori Moriyono
 Genome Research Group
 National Institute of Radiological Sciences
 9-1, Anagawa-4-chome, Inage-Ku, Chiba 263-8555, Japan
 Email: moriyono@nirs.go.jp.
 Location/Qualifiers
 1.184
 /organism="Schizosaccharomyces pombe"
 /mol_type="mRNA"
 /strain="972"
 /db_xref="taxon:4896"
 /clone="spc10423"
 /sex="h minus"
 /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
 /note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"

BASE COUNT 48 a 42 c 38 g 56 t

ORIGIN

Query Match 100.0%; Score 35; DB 9; Length 184;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CTAGTCGCATAGTTATGTTAGTACGACG 35
 |||||
 68 CTAGTCGCATAGTTATGTTAGTACGACG 102

Qy

FEATURES
 source

LOCUS AU010834 184 bp mRNA linear EST 31-JUL-1998
 DEFINITION AU010834 Schizosaccharomyces pombe late log phase cDNA
 Schizosaccharomyces pombe cDNA clone spc10423, mRNA sequence.
 ACCESSION AU010834
 VERSION AU010834.1 GI:3347514
 KEYWORDS EST
 SOURCE Schizosaccharomyces pombe (fission yeast)
 ORGANISM Schizosaccharomyces pombe
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 Schizosaccharomycetales; Schizosaccharomycetaceae;
 Schizosaccharomyces.
 REFERENCE 1 (bases 1 to 184)
 AUTHORS Moriyono,M. and Mita,K.
 TITLE Identification of expressed sequence tags of Schizosaccharomyces pombe

JOURNAL
 COMMENT Unpublished
 Contact: Mitsunori Moriyono
 Genome Research Group
 National Institute of Radiological Sciences
 9-1, Anagawa-4-chome, Inage-Ku, Chiba 263-8555, Japan
 Email: moriyono@nirs.go.jp.
 Location/Qualifiers
 1.184
 /organism="Schizosaccharomyces pombe"
 /mol_type="mRNA"
 /strain="972"
 /db_xref="taxon:4896"
 /clone="spc10423"
 /sex="h minus"
 /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
 /note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"

BASE COUNT 48 a 42 c 38 g 56 t

ORIGIN

Query Match 100.0%; Score 35; DB 9; Length 184;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CTAGTCGCATAGTTATGTTAGTACGACG 35
 |||||
 68 CTAGTCGCATAGTTATGTTAGTACGACG 102

Qy

FEATURES
 source

RESULT 7
LOCUS AU010835 184 bp mRNA linear EST 31-JUL-1998
DEFINITION AU010835 Schizosaccharomyces pombe late log phase cDNA
ACCESSION AU010835 Schizosaccharomyces pombe cDNA clone spc10424, mRNA sequence.
VERSION AU010835
KEYWORDS EST.
SOURCE Schizosaccharomyces pombe (fission yeast)
ORGANISM Schizosaccharomyces pombe
REFERENCE Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
AUTHORS 1 (bases 1 to 184)
TITLE Morimyo,M. and Mita,K.
FEATURES Identification of expressed sequence tags of Schizosaccharomyces pombe
JOURNAL Unpublished
COMMENT Contact: Mitsunori Morimyo
 Genome Research Group
 National Institute of Radiological Sciences
 9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
 Email: morimyo@nirs.go.jp.
FEATURES Location/Qualifiers
 1..184
 /organism="Schizosaccharomyces pombe"
 /mol_type="mRNA"
 /strain="972"
 /db_xref="taxon:4896"
 /clone="spc10424"
 /sex="h minus"
 /note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"
BASE COUNT 48 a 42 c 38 g 56 t
ORIGIN

Query Match 100.0%; Score 35; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTAGTCGCATAGTTTATGTTAGACTACGACG 35
 ||||||||||||||||||||||||||||||||
Db 68 CTAGTCGCATAGTTTATGTTAGACTACGACG 102

RESULT 8
LOCUS AU011658 195 bp mRNA linear EST 03-AUG-1998
DEFINITION AU011658 Schizosaccharomyces pombe late log phase cDNA
ACCESSION AU011658 Schizosaccharomyces pombe cDNA clone spc11806, mRNA sequence.
VERSION AU011658
KEYWORDS EST.
SOURCE Schizosaccharomyces pombe (fission yeast)
ORGANISM Schizosaccharomyces pombe
REFERENCE Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
AUTHORS 1 (bases 1 to 195)
TITLE Morimyo,M. and Mita,K.
FEATURES Identification of expressed sequence tags of Schizosaccharomyces pombe
JOURNAL Unpublished
COMMENT Contact: Mitsunori Morimyo
 Genome Research Group
 National Institute of Radiological Sciences

FEATURES 9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
SOURCE Email: morimyo@nirs.go.jp.
 Location/Qualifiers
 1..195
 /organism="Schizosaccharomyces pombe"
 /mol_type="mRNA"
 /strain="972"
 /db_xref="taxon:4896"
 /clone="spc11806"
 /sex="h minus"
 /note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"
BASE COUNT 63 a 36 c 43 g 52 t 1 others
ORIGIN

Query Match 100.0%; Score 35; DB 9; Length 195;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTAGTCGCATAGTTTATGTTAGACTACGACG 35
 ||||||||||||||||||||||||||||||||
Db 138 CTAGTCGCATAGTTTATGTTAGACTACGACG 104

RESULT 9
LOCUS AU011659 195 bp mRNA linear EST 03-AUG-1998
DEFINITION AU011659 Schizosaccharomyces pombe late log phase cDNA
ACCESSION AU011659 Schizosaccharomyces pombe cDNA clone spc11807, mRNA sequence.
VERSION AU011659
KEYWORDS EST.
SOURCE Schizosaccharomyces pombe (fission yeast)
ORGANISM Schizosaccharomyces pombe
REFERENCE Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
AUTHORS 1 (bases 1 to 195)
TITLE Morimyo,M. and Mita,K.
FEATURES Identification of expressed sequence tags of Schizosaccharomyces pombe
JOURNAL Unpublished
COMMENT Contact: Mitsunori Morimyo
 Genome Research Group
 National Institute of Radiological Sciences
 9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
 Email: morimyo@nirs.go.jp.
FEATURES Location/Qualifiers
 1..195
 /organism="Schizosaccharomyces pombe"
 /mol_type="mRNA"
 /strain="972"
 /db_xref="taxon:4896"
 /clone="spc11807"
 /sex="h minus"
 /note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"
BASE COUNT 63 a 36 c 43 g 52 t 1 others
ORIGIN

Qy 1 CTAGTCGGCATAGTTATGTTAAGACTACGACGG 35
LOCUS 138 CTAGTCGGCATAGTTATGTTAAGACTACGACGG 104

RESULT 10
AU007372/c 196 bp mRNA linear EST 31-JUL-1998
DEFINITION AU007372 Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe cDNA clone spc01850, mRNA sequence.
ACCESSION AU007372
VERSION AU007372.1 GI:3343830
SOURCE EST.
ORGANISM Schizosaccharomyces pombe (fission yeast)
Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
1 (bases 1 to 196)
Moriyomo,M. and Mita,K.
Identification of expressed sequence tags of Schizosaccharomyces
pombe
JOURNAL Unpublished
COMMENT Contact: Mitsunuki Moriyomo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: moriyom@nirs.go.jp.
Location/Qualifiers
1. 196
/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/strain="972"
/db_xref="taxon:4896"
/clone="spc01850"
/sex="h minus"
/note="Vector: M13mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the SmaI site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, <http://www.nirs.go.jp>)"

BASE COUNT 59 a 37 c 45 g 55 t

ORIGIN

Query Match 100.0%; Score 35; DB 9; Length 196;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAGTCGGCATAGTTATGTTAAGACTACGACGG 35
Db 129 CTAGTCGGCATAGTTATGTTAAGACTACGACGG 95

RESULT 11
AU009140 197 bp mRNA linear EST 31-JUL-1998
LOCUS AU009140 Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe cDNA clone spc04530, mRNA sequence.
ACCESSION AU009140
VERSION AU009140.1 GI:3345820
SOURCE EST.
ORGANISM Schizosaccharomyces pombe (fission yeast)
Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
1 (bases 1 to 197)
Moriyomo,M. and Mita,K.
Identification of expressed sequence tags of Schizosaccharomyces
pombe

JOURNAL Unpublished
COMMENT Contact: Mitsunuki Moriyomo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: moriyom@nirs.go.jp.
Location/Qualifiers
1. 197
/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/strain="972"
/db_xref="taxon:4896"
/clone="spc04530"
/sex="h minus"
/note="Vector: M13mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the SmaI site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, <http://www.nirs.go.jp>)"

BASE COUNT 55 a 45 c 38 g 59 t

ORIGIN

Query Match 100.0%; Score 35; DB 9; Length 197;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAGTCGGCATAGTTATGTTAAGACTACGACGG 35
Db 68 CTAGTCGGCATAGTTATGTTAAGACTACGACGG 102

RESULT 12
A2931573/c 224 bp DNA linear GSS 01-APR-2001
LOCUS A2931573 474.dhz86c05.s1 Saccharomyces unisporus NRRL Y-1556 Saccharomyces
unisporus genomic clone 474.dhz86c05.s1, genomic survey sequence.
ACCESSION A2931573
VERSION A2931573.1 GI:13502484
KEYWORDS GSS.
SOURCE Saccharomyces unisporus
ORGANISM Saccharomyces unisporus
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
1 (bases 1 to 224)
Cliften,P.F., Hillier,L.W., Fulton,L., Graves,T., Miner,T., Glsh
M.R., Waterston,R.H. and Johnston,M.
Surveying Saccharomyces genomes to identify functional elements by
comparative DNA sequence analysis
JOURNAL Unpublished
COMMENT Contact: Johnston M
Department of Genetics
Washington University Medical School
Box 8232, 4566 Scott Ave., St. Louis, MO 63110, USA
Tel: 314 362 2735
Fax: 314 362 7835
Email: mjgenetics.wustl.edu
Class: random plasmid subclone.
Location/Qualifiers
1. 224
/organism="Saccharomyces unisporus"
/mol_type="genomic DNA"
/strain="NRRL Y-1556 (CBS 398)"
/db_xref="taxon:27294"
/clone="474.dhz86c05.s1"
/note="Random genomic sequence"

BASE COUNT 67 a 40 c 60 g 57 t

ORIGIN

Query Match 100.0%; Score 35; DB 28; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.00016;

Matches 35: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTAGTCGGCATAGTTATGTTAGACTACGACG 35
 |||||||||||||||||||||||||||||||||||

Db 111 CTAGTCGGCATAGTTATGTTAGACTACGACG 77

RESULT 13
 A0007492 237 bp mRNA linear EST 31-JUL-1998
 LOCUS A0007492 Schizosaccharomyces pombe late log phase cDNA
 DEFINITION A0007492 Schizosaccharomyces pombe cDNA clone spc02102, mRNA sequence.
 ACCESSION A0007492
 VERSION A0007492.1 GI:3343950
 KEYWORDS EST.
 SOURCE Schizosaccharomyces pombe (filson yeast)
 ORGANISM Schizosaccharomyces pombe (filson yeast)
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 Schizosaccharomycetales; Schizosaccharomycetaceae;
 Schizosaccharomyces.
 1 (bases 1 to 237)
 Morimyo M. and Mita K.
 REFERENCE Identification of expressed sequence tags of Schizosaccharomyces
 AUTHORS Morimyo M. and Mita K.
 TITLE Identification of expressed sequence tags of Schizosaccharomyces
 JOURNAL Unpublished
 COMMENT Contact: Mitsuoki Morimyo
 Genome Research Group
 National Institute of Radiological Sciences
 9-1, Arinaga-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
 Email: morimyo@nirs.go.jp.
 Location/Qualifiers
 1..237
 /organism="Schizosaccharomyces pombe"
 /mol_type="mRNA"
 /strain="972"
 /db_xref="taxon:4896"
 /clone="spc02102"
 /sex="h minus"
 /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
 /note="Vector: M13mp19. The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, <http://www.nirs.go.jp>)"

BASE COUNT 65 a 58 c 44 g 67 t 3 others

ORIGIN

Query Match 100.0%; Score 35; DB 9; Length 237;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTAGTCGGCATAGTTATGTTAGACTACGACG 35
 |||||||||||||||||||||||||||||||||||

Db 68 CTAGTCGGCATAGTTATGTTAGACTACGACG 102

RESULT 14
 A1904526 296 bp mRNA linear EST 30-MAR-2000
 LOCUS A1904526 PM-BT057-290199-289 BT057 Homo sapiens cDNA, mRNA sequence.
 DEFINITION A1904526
 ACCESSION A1904526.1 GI:6494913
 VERSION A1904526.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 296)
 Dias Neto E., Garcia Correa R., Verjovski-Almeida S., Briones M.R., Nagai M.A., da Silva W. Jr., Zago M.A., Bordin S., Costa F.F., Goldman G.H., Carvalho A.F., Matsukuma A., Bala G.S., Simpson D.H., Brunstein A., de Oliveira P.S., Bucher P., Jongeneel C.V., O'Hare
 Brunstein A., de Oliveira P.S., Bucher P., Jongeneel C.V., O'Hare

TITLE
 JOURNAL MEDLINE
 PUBMED
 COMMENT

CONTACT: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/seq/gethtml.pl?cl=PM&cl=PM-BT057-289.html>)
 Seq primer: puc 18 forward.
 Location/Qualifiers
 1..296
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /sex="female"
 /dev_stage="Adult"
 /clone_lib="BT057"
 /note="Organ: breast; Vector: puc18; Site:1; SmaI; Site:2; SmaI; A mini-library was made by cloning products derived from ORESTES PCR (O.S. Letters Patent Application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 88 a 36 c 78 g 74 t

ORIGIN

Query Match 100.0%; Score 35; DB 9; Length 296;
 Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTAGTCGGCATAGTTATGTTAGACTACGACG 35
 |||||||||||||||||||||||||||||||||||

Db 128 CTAGTCGGCATAGTTATGTTAGACTACGACG 94

RESULT 15
 A1904469 316 bp mRNA linear EST 30-MAR-2000
 LOCUS A1904469 PM-BT057-100299-389 BT057 Homo sapiens cDNA, mRNA sequence.
 DEFINITION A1904469
 ACCESSION A1904469.1 GI:6494856
 VERSION A1904469.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 316)
 Dias Neto E., Garcia Correa R., Verjovski-Almeida S., Briones M.R., Nagai M.A., da Silva W. Jr., Zago M.A., Bordin S., Costa F.F., Goldman G.H., Carvalho A.F., Matsukuma A., Bala G.S., Simpson D.H., Brunstein A., de Oliveira P.S., Bucher P., Jongeneel C.V., O'Hare
 Brunstein A., de Oliveira P.S., Bucher P., Jongeneel C.V., O'Hare

TITLE
 JOURNAL MEDLINE
 PUBMED
 COMMENT

CONTACT: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/seq/gethtml.pl?tl=PM&t2=PM-BT057-389.html>
6t3-1002996t4-1)

Seq primer: puc 18 forward.

Location/Qualifiers

FEATURES

source

1. .316

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/sex="female"

/dev_stage="Adult"

/clone_lib="BT057"

/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:

SmaI; A mini-library was made by cloning products derived

from ORESTES PCR (U.S. Letters Patent application No. 196

,716 - Ludwig Institute for Cancer Research) profiles

into the pUC 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

74 a 87 c 66 g 89 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 35; DB 9; Length 316;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGTCGGCATAGTTATGCTTAAGACTACGACGG 35

Db 190 CTAGTCGGCATAGTTATGCTTAAGACTACGACGG 224

Search completed: August 7, 2003, 00:28:29
Job time : 1896.28 secs

PT of C. albicans, C. dubliniensis, C. viswanathii, C. parapsilosis in test
sample -
PS Claim 2; Page 26; 33pp; English.
XX
CC The present sequence is that of helper oligonucleotide
CC CALA1006, which binds target Candida spp. ribosomal RNA molecules
CC at a site immediately adjacent to probe CALA1038 (see AA170913).
CC The helper oligonucleotide promotes the highly specific
CC hybridisation of CALA1038 probe to a sequence found in the 18S rRNA
CC of Candida albicans, Candida tropicalis, Candida dubliniensis,
CC Candida viswanathii and Candida tropicalis. Probe CALA1038 can
CC distinguish these Candida species from their known phylogenetically
CC nearest neighbours, and is useful for their detection and
CC quantitation. The Tm of interaction between probe and C. albicans
CC rRNA increased from 57.8 to 62.2 degrees C when the helper
CC oligonucleotide was added to the hybridisation reaction, and
CC increased to 63.2 degrees C when another helper oligonucleotide,
CC CALA1066 (see AA170912), was also included.
XX
SQ Sequence 35 BP; 9 A; 6 C; 10 G; 10 T; 0 other;
Query Match 100.0%; Score 35; DB 24; Length 35;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTAGTCGCATAGTTATGTTAGACTACGACG 35
DB 1 CTAGTCGCATAGTTATGTTAGACTACGACG 35
RESULT 2
AAA94981/C
ID AAA94981 standard; DNA; 51 BP.
XX
AC AAA94981;
XX
DT 10-JAN-2001 (first entry)
XX
DE S. arleticantis small ribosomal subunit nucleotide sequence fragment #81.
XX
KW Small ribosomal subunit; SRSU; Equine protozoal myeloencephalitis;
XX EPM; diagnosis; ds.
XX
OS S. arleticantis.
XX
PN US6110665-A.
XX
PD 29-AUG-2000.
XX
PE 14-FEB-1995; 95US-0388029.
XX
PR 14-FEB-1995; 95US-0388029.
XX
PA (KENT) UNIV KENTUCKY RES FOUND.
XX
PI Fenger CK, Gajadhar AA, Dubey JP, Granstrom DE;
XX WPI; 2000-586347/55.
XX
DR
XX
PT Sarcocystis neuropa diagnostic primer, useful for in vitro diagnostic
PT testing for Equine protozoal myeloencephalitis, i.e. for diagnosing the
PT presence of S. neuropa in equine blood or cerebrospinal fluid -
PS Disclosure; Fig 1; 41pp; English.
XX
CC The present invention relates to a diagnostic primer from positions
CC 1470-1487 of the small ribosomal subunit of Sarcocystis neuropa. This
CC primer is unique to the S. neuropa species. The primer is useful for
CC diagnostic tests for Equine protozoal myeloencephalitis (EPM) where
CC the presence of S. neuropa is indicative of EPM. To find a
CC sequence unique to S. neuropa small ribosomal subunit sequences from
CC S. neuropa, S. muris, S. gigantea, T. gondii, S. capicantis, S.

CC arleticantis, S. cruzi, S. tenella, E. tenella and C. parvum were
CC compared. The present sequence is a fragment of the small ribosomal
CC subunit used in this comparison.
XX
SQ Sequence 51 BP; 17 A; 12 C; 11 G; 11 T; 0 other;
Query Match 100.0%; Score 35; DB 21; Length 51;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTAGTCGCATAGTTATGTTAGACTACGACG 35
DB 49 CTAGTCGCATAGTTATGTTAGACTACGACG 15
RESULT 3
AAA94985/C
ID AAA94985 standard; DNA; 51 BP.
XX
AC AAA94985;
XX
DT 10-JAN-2001 (first entry)
XX
DE T. gondii small ribosomal subunit nucleotide sequence fragment #85.
XX
KW Small ribosomal subunit; SRSU; Equine protozoal myeloencephalitis;
XX EPM; diagnosis; ds.
XX
OS T. gondii.
XX
PN US6110665-A.
XX
PD 29-AUG-2000.
XX
PE 14-FEB-1995; 95US-0388029.
XX
PR 14-FEB-1995; 95US-0388029.
XX
PA (KENT) UNIV KENTUCKY RES FOUND.
XX
PI Fenger CK, Gajadhar AA, Dubey JP, Granstrom DE;
XX WPI; 2000-586347/55.
XX
DR
XX
PT Sarcocystis neuropa diagnostic primer, useful for in vitro diagnostic
PT testing for Equine protozoal myeloencephalitis, i.e. for diagnosing the
PT presence of S. neuropa in equine blood or cerebrospinal fluid -
PS Disclosure; Fig 1; 41pp; English.
XX
CC The present invention relates to a diagnostic primer from positions
CC 1470-1487 of the small ribosomal subunit of Sarcocystis neuropa. This
CC primer is unique to the S. neuropa species. The primer is useful for
CC diagnostic tests for Equine protozoal myeloencephalitis (EPM) where
CC the presence of S. neuropa is indicative of EPM. To find a
CC sequence unique to S. neuropa small ribosomal subunit sequences from
CC S. neuropa, S. muris, S. gigantea, T. gondii, S. capicantis, S.
CC arleticantis, S. cruzi, S. tenella, E. tenella and C. parvum were
CC compared. The present sequence is a fragment of the small ribosomal
CC subunit used in this comparison.
XX
SQ Sequence 51 BP; 17 A; 12 C; 11 G; 11 T; 0 other;
Query Match 100.0%; Score 35; DB 21; Length 51;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTAGTCGCATAGTTATGTTAGACTACGACG 35
DB 49 CTAGTCGCATAGTTATGTTAGACTACGACG 15
RESULT 4

PS Disclosure; Fig 1; 41pp; English.
XX
CC The present invention relates to a diagnostic primer from positions
CC 1470-1487 of the small ribosomal subunit of *Sarcocystis neurona*. This
CC primer is unique to the *S. neurona* species. The primer is useful for
CC diagnostic tests for Equine protozoal myeloencephalitis (EPM) where
CC the presence of *S. neurona* is indicative of EPM. To find a
CC sequence unique to *S. neurona* small ribosomal subunit sequences from
CC *S. neurona*, *S. muris*, *S. gigantea*, *T. gondii*, *S. capicantus*, *S.*
CC *arieticanis*, *S. cruzi*, *S. tenella*, *E. tenella* and *C. parvum* were
CC compared. The present sequence is a fragment of the small ribosomal
CC subunit used in this comparison.
SQ Sequence 52 BP; 17 A; 12 C; 11 G; 11 T; 1 other;
XX
Query Match 100.0%; Score 35; DB 21; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTAGTCGGCATAGTTATGTTAGTAACTACGACGG 35
Db 50 CTAGTCGGCATAGTTATGTTAGTAACTACGACGG 16
XX
RESULT 7
AAA94983/c
ID AAA94983 standard; DNA; 52 BP.
XX
AC AAA94983;
XX
DT 10-JAN-2001 (first entry)
XX
DE *S. gigantea* small ribosomal subunit nucleotide sequence fragment #83.
XX
KW Small ribosomal subunit; SRSU; Equine protozoal myeloencephalitis;
XX EPM; diagnosis; ds.
XX
OS *S. gigantea*.
XX
PN US6110665-A.
XX
PD 29-AUG-2000.
XX
PF 14-FEB-1995; 95US-0388029.
XX
PR 14-FEB-1995; 95US-0388029.
XX
PA (KENT) UNIV KENTUCKY RES FOUND.
XX
PI Fenger CK, Gajadhar AA, Dubey JP, Granstrom DE;
XX WPI; 2000-586347/55.
XX
DR
XX
PT Sarcocystis *neurona* diagnostic primer, useful for in vitro diagnostic
PT testing for Equine protozoal myeloencephalitis, i.e. for diagnosing the
PT presence of *S. neurona* in equine blood or cerebrospinal fluid -
XX
XX Disclosure; Fig 1; 41pp; English.
PS
XX
CC The present invention relates to a diagnostic primer from positions
CC 1470-1487 of the small ribosomal subunit of *Sarcocystis neurona*. This
CC primer is unique to the *S. neurona* species. The primer is useful for
CC diagnostic tests for Equine protozoal myeloencephalitis (EPM) where
CC the presence of *S. neurona* is indicative of EPM. To find a
CC sequence unique to *S. neurona* small ribosomal subunit sequences from
CC *S. neurona*, *S. muris*, *S. gigantea*, *T. gondii*, *S. capicantus*, *S.*
CC *arieticanis*, *S. cruzi*, *S. tenella*, *E. tenella* and *C. parvum* were
CC compared. The present sequence is a fragment of the small ribosomal
CC subunit used in this comparison.
SQ Sequence 52 BP; 18 A; 12 C; 11 G; 11 T; 0 other;
XX
Query Match 100.0%; Score 35; DB 21; Length 52;
XX

Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTAGTCGGCATAGTTATGTTAGTAACTACGACGG 35
Db 50 CTAGTCGGCATAGTTATGTTAGTAACTACGACGG 16
XX
RESULT 8
ABA99904
ID ABA99904 standard; DNA; 75 BP.
XX
AC ABA99904;
XX
DT 17-JUN-2002 (first entry)
XX
DE *C. albicans* 18S RNA detecting multiplex probe SEQ ID 6.
XX
KW 18S RNA; multiplex PCR; PCR; probe; detection; amplification;
KW fungal infection; pathogenic; ss.
XX
OS *Candida albicans*.
XX
PN WO200227021-A2.
XX
PD 04-APR-2002.
XX
PF 24-SEP-2001; 2001WO-EP11023.
XX
PR 26-SEP-2000; 2000DE-1048009.
XX
PA (CYTO-) CYTONE GMBH & CO KG.
XX
PI Boettger EC, Rosenau J, Kirschner P, Jack T;
XX WPI; 2002-330101/36.
XX
DR
XX
PT Multiplex amplification for detecting fungal infection, selective for
PT clinically important strains of *Candida* and *Aspergillus*, comprises
PT amplifying a region of the 18S RNA gene -
XX
XX Claim 13; Page 27; 27pp; German.
XX
PS
XX
CC This invention describes a novel multiplex amplification reaction for
CC detecting clinically relevant fungal infections by amplifying a region of
CC the 18S RNA gene, where either sequences from pathogenic *Candida* and
CC *Aspergillus* species are amplified. The method is quick, simple and
CC sensitive, and can detect all clinically important *Candida* and
CC *Aspergillus* species, but generally it does not detect species commonly
CC present in laboratories as contaminants (avoiding false positive
CC results). The detection limit is 3-20 cells/10 ml of blood, depending on
CC the detection method used. This sequence represents a probe used in
CC the method of the invention.
XX
SQ Sequence 75 BP; 15 A; 20 C; 14 G; 25 T; 1 other;
XX
XX
Query Match 100.0%; Score 35; DB 24; Length 75;
Best Local Similarity 100.0%; Pred. No. 4.9e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTAGTCGGCATAGTTATGTTAGTAACTACGACGG 35
Db 8 CTAGTCGGCATAGTTATGTTAGTAACTACGACGG 42
XX
RESULT 9
AAI70915
ID AAI70915 standard; DNA; 113 BP.
XX
AC AAI70915;
XX
DT 12-MAR-2002 (first entry)
XX

DE Candida species 18S ribosomal DNA probe domain.
XX
KW Candida albicans; Candida tropicalis; Candida dubliniensis;
KW Candida viswanathii; Candida parapsilosis; detection; probe; ss.
XX
OS Candida albicans.
XX
PN WO200183821-A2.
XX
PD 08-NOV-2001.
XX
PF 01-MAY-2001; 2001WO-US13884.
XX
PR 01-MAY-2000; 2000US-201249P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Hogan JJ, Gordon PC;
XX
DR WPI; 2002-066537/09.
XX
PT Novel oligonucleotide sequences that are fully complementary to
PT ribosomal RNA or DNA of Candida species, useful for detecting presence
PT of C.albicans, C.dubliniensis, C.viswanathii, C.parapsilosis in test
PT sample -
XX
PS Claim 1; Page 32; 33pp; English.
XX
CC The present sequence is that of DNA corresponding to a unique
CC segment (see AAI70916) of the 18S ribosomal RNA of Candida albicans,
CC Candida tropicalis, Candida dubliniensis, Candida viswanathii and
CC oligonucleotides (see AAI70909-14) correspond to a portion of this
CC sequence or its complement. The probes are highly specific, and can
CC distinguish these Candida species from their known phylogenetically
CC nearest neighbours. They are useful for detection and quantitation.
XX
SQ Sequence 113 BP; 35 A; 27 C; 23 G; 28 T; 0 other;
XX
Query Match 100.0%; Score 35; DB 24; Length 113;
Best Local Similarity 100.0%; Pred. No. 5,2e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTAGTCGCATAGTTATGTTAGTAACTACGACG 35
Db 70 CTAGTCGCATAGTTATGTTAGTAACTACGACG 104
XX
RESULT 10
AAI70916/C
ID AAI70916 standard; rRNA; 113 BP.
XX
AC AAI70916;
XX
DT 12-MAR-2002 (first entry)
XX
DE Candida species 18S ribosomal RNA probe domain.
XX
KW Candida albicans; Candida tropicalis; Candida dubliniensis;
KW Candida viswanathii; Candida parapsilosis; detection; probe; ss.
XX
OS Candida albicans.
XX
PN WO200183821-A2.
XX
PD 08-NOV-2001.
XX
PF 01-MAY-2001; 2001WO-US13884.
XX
PR 01-MAY-2000; 2000US-201249P.
XX
PA (GENP-) GEN-PROBE INC.
XX

PI Hogan JJ, Gordon PC;
XX
DR WPI; 2002-066537/09.
XX
PT Novel oligonucleotide sequences that are fully complementary to
PT ribosomal RNA or DNA of Candida species, useful for detecting presence
PT of C.albicans, C.dubliniensis, C.viswanathii, C.parapsilosis in test
PT sample -
XX
PS Disclosure; Page 32; 33pp; English.
XX
CC The present sequence is that of a unique segment of the 18S
CC ribosomal RNA of Candida albicans, Candida tropicalis,
CC Candida dubliniensis, Candida viswanathii and Candida tropicalis.
CC Claimed hybridisation probes and helper oligonucleotides (see
CC AAI70909-14) correspond to a portion of this sequence or its
CC complement. The probes are highly specific, and can distinguish
CC these Candida species from their known phylogenetically nearest
CC neighbours. They are useful for detection and quantitation.
XX
SQ Sequence 113 BP; 28 A; 23 C; 27 G; 35 U; 0 other;
XX
Query Match 100.0%; Score 35; DB 24; Length 113;
Best Local Similarity 100.0%; Pred. No. 5,2e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTAGTCGCATAGTTATGTTAGTAACTACGACG 35
Db 44 CTAGTCGCATAGTTATGTTAGTAACTACGACG 10
XX
RESULT 11
AAH21226/C
ID AAH21226 standard; DNA; 421 BP.
XX
AC AAH21226;
XX
DT 13-SEP-2001 (first entry)
XX
DE C. krusei 16S rRNA DNA fragment YSARSUD.
XX
KW Hybridization; diagnosis; bacterial infection; sepsis; fungal infection;
KW food monitoring; water monitoring; veterinary; forensic; primer; probe;
KW detection; ss.
XX
OS Candida krusei.
XX
PN WO200148237-A2.
XX
PD 05-JUL-2001.
XX
PF 27-DEC-2000; 2000WO-DE04610.
XX
PR 23-DEC-1999; 99DE-1062895.
PR 31-MAY-2000; 2000DE-1027113.
XX
PA (HOEF/) HOEF A.
PA (STUE/) STUEBER F.
PI Hoeft A, Stueber F;
XX
DR WPI; 2001-425677/45.
XX
PT Rapid determination of microbial nucleic acid, useful e.g. for
PT diagnosing bacterial infections, by analysis of temperature-dependent
PT hybridization with oligonucleotides -
XX
PS Disclosure; Figure 13; 57pp; German.
XX
CC This invention describes a novel method for detecting microbial DNA/RNA
CC (I) by concentrating (I) from a sample, adding at least one labeled
CC oligonucleotide (ON), performing temperature-dependent hybridization and
CC determining (I) from the physical properties of the (I)-ON complex, e.g.

CC the temperature dependence of hybridization. The method is used for rapid
CC determination of microbial genomic RNA or DNA, particularly for diagnosis
CC of bacterial infections (e.g. sepsis) or fungal infections (particularly
CC in intensive care patients), also for monitoring food and water, and for
CC veterinary or forensic investigations. The method provides quick
CC (typically less than 3 hours) quantitative and qualitative
CC determination/identification of microbial nucleic acid. It is very
CC sensitive, allowing early diagnosis of infection. AAH21160-AAH21231
CC represent primers and probes used to illustrate the method of the
CC invention.

CC
XX
SQ Sequence 421 BP; 109 A; 88 C; 115 G; 104 T; 5 other;

Query Match 100.0%; Score 35; DB 22; Length 421;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTAGTCGCATAGTTATGTTAAGACTACGACGG 35
DB 376 CTAGTCGCATAGTTATGTTAAGACTACGACGG 342
|||||

RESULT 12
AAH21229/c
ID AAH21229 standard; DNA; 429 BP.
XX
AC AAH21229;
XX
DT 13-SEP-2001 (first entry)
XX
DE C. tropicalis 16S rRNA DNA fragment YSASRSUG.
XX
KM Hybridization; diagnosis; bacterial infection; sepsis; fungal infection;
KM food monitoring; water monitoring; veterinary; forensic; primer; probe;
KM detection; ss.
XX
OS Candida tropicalis.
XX
PN WO200148237-A2.
XX
PD 05-JUL-2001.
XX
PE 27-DEC-2000; 2000WO-DE04610.
XX
PR 23-DEC-1999; 99DE-1062895.
PR 31-MAY-2000; 2000DE-1027113.
XX
PA (HOEF/) HOEFT A.
PA (STUE/) STUEBER F.
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PI Hoeft A, Stueber F;
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DR WPI; 2001-425677/45.
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PT Rapid determination of microbial nucleic acid, useful e.g. for
PT diagnosing bacterial infections, by analysis of temperature-dependent
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PS Disclosure; Figure 13; 57pp; German.
XX
CC This invention describes a novel method for detecting microbial DNA/RNA
CC (1) by concentrating (I) from a sample, adding at least one labeled
CC oligonucleotide (ON), performing temperature-dependent hybridization and
CC determining (II) from the physical properties of the (I)-ON complex, e.g.
CC the temperature dependence of hybridization. The method is used for rapid
CC determination of microbial genomic RNA or DNA, particularly for diagnosis
CC of bacterial infections (e.g. sepsis) or fungal infections (particularly
CC in intensive care patients), also for monitoring food and water, and for
CC veterinary or forensic investigations. The method provides quick
CC (typically less than 3 hours) quantitative and qualitative
CC determination/identification of microbial nucleic acid. It is very
CC sensitive, allowing early diagnosis of infection. AAH21160-AAH21231
CC represent primers and probes used to illustrate the method of the

CC invention.
XX
SQ Sequence 429 BP; 114 A; 85 C; 109 G; 119 T; 2 other;

Query Match 100.0%; Score 35; DB 22; Length 429;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTAGTCGCATAGTTATGTTAAGACTACGACGG 35
DB 380 CTAGTCGCATAGTTATGTTAAGACTACGACGG 346
|||||

RESULT 13
AAH21230/c
ID AAH21230 standard; DNA; 431 BP.
XX
AC AAH21230;
XX
DT 13-SEP-2001 (first entry)
XX
DE C. albicans 16S rRNA DNA fragment YSASRSUA.
XX
KM Hybridization; diagnosis; bacterial infection; sepsis; fungal infection;
KM food monitoring; water monitoring; veterinary; forensic; primer; probe;
KM detection; ss.
XX
OS Candida albicans.
XX
PN WO200148237-A2.
XX
PD 05-JUL-2001.
XX
PE 27-DEC-2000; 2000WO-DE04610.
XX
PR 23-DEC-1999; 99DE-1062895.
PR 31-MAY-2000; 2000DE-1027113.
XX
PA (HOEF/) HOEFT A.
PA (STUE/) STUEBER F.
XX
PI Hoeft A, Stueber F;
XX
DR WPI; 2001-425677/45.
XX
PT Rapid determination of microbial nucleic acid, useful e.g. for
PT diagnosing bacterial infections, by analysis of temperature-dependent
PT hybridization with oligonucleotides
XX
PS Disclosure; Figure 13; 57pp; German.
XX
CC This invention describes a novel method for detecting microbial DNA/RNA
CC (1) by concentrating (I) from a sample, adding at least one labeled
CC oligonucleotide (ON), performing temperature-dependent hybridization and
CC determining (II) from the physical properties of the (I)-ON complex, e.g.
CC the temperature dependence of hybridization. The method is used for rapid
CC determination of microbial genomic RNA or DNA, particularly for diagnosis
CC of bacterial infections (e.g. sepsis) or fungal infections (particularly
CC in intensive care patients), also for monitoring food and water, and for
CC veterinary or forensic investigations. The method provides quick
CC (typically less than 3 hours) quantitative and qualitative
CC determination/identification of microbial nucleic acid. It is very
CC sensitive, allowing early diagnosis of infection. AAH21160-AAH21231
CC represent primers and probes used to illustrate the method of the

Query Match 100.0%; Score 35; DB 22; Length 431;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTAGTCGCATAGTTATGTTAAGACTACGACGG 35

DB 382 CTAGTCGCAATGTTATGTTAAGACTACGACG 348

RESULT 14

AAH21228/C
ID AAH21228 standard; DNA; 432 BP.

AAH21228;

13-SEP-2001 (first entry)

C. parapsilosis 16S rRNA DNA fragment YSASRSUF.

Hybridization; diagnosis; bacterial infection; sepsis; fungal infection;
food monitoring; water monitoring; veterinary; forensic; primer; probe;
detection; ss.

Candida parapsilosis.

MO200148237-A2.

05-JUL-2001.

27-DEC-2000; 2000MO-DE04610.

23-DEC-1999; 99DE-1062895.

31-MAY-2000; 2000DE-1027113.

(HOEF/) HOEFT A.
(STUE/) STUEBER F.

Hoeft A, Stueber F;

WPI: 2001-425677/45.

Rapid determination of microbial nucleic acid, useful e.g. for
diagnosing bacterial infections, by analysis of temperature-dependent
hybridization with oligonucleotides

Disclosure; Figure 13; 57pp; German.

This invention describes a novel method for detecting microbial DNA/RNA
(I) by concentrating (I) from a sample, adding at least one labeled
oligonucleotide (ON), performing temperature-dependent hybridization and
determining (I) from the physical properties of the (I)-ON complex, e.g.
the temperature dependence of hybridization. The method is used for rapid
determination of microbial genomic RNA or DNA, particularly for diagnosis
of bacterial infections (e.g. sepsis) or fungal infections (particularly
in intensive care patients), also for monitoring food and water, and for
veterinary or forensic investigations. The method provides quick
determination/identification of microbial nucleic acid. It is very
sensitive, allowing early diagnosis of infection. AAH21160-AAH21231
represent primers and probes used to illustrate the method of the
invention.

Sequence 432 BP; 114 A; 86 C; 110 G; 121 T; 1 other;

Query Match 100.0%; Score 35; DB 22; Length 432;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTAGTCGCAATGTTATGTTAAGACTACGACG 35
383 CTAGTCGCAATGTTATGTTAAGACTACGACG 349

RESULT 15
AAH21227/C
ID AAH21227 standard; DNA; 444 BP.
AAH21227;

13-SEP-2001 (first entry)

T. glabrata 16S rRNA DNA fragment YLSRSUA.

Hybridization; diagnosis; bacterial infection; sepsis; fungal infection;
food monitoring; water monitoring; veterinary; forensic; primer; probe;
detection; ss.

Torulopsis glabrata.

MO200148237-A2.

05-JUL-2001.

27-DEC-2000; 2000MO-DE04610.

23-DEC-1999; 99DE-1062895.

31-MAY-2000; 2000DE-1027113.

(HOEF/) HOEFT A.
(STUE/) STUEBER F.

Hoeft A, Stueber F;

WPI: 2001-425677/45.

Rapid determination of microbial nucleic acid, useful e.g. for
diagnosing bacterial infections, by analysis of temperature-dependent
hybridization with oligonucleotides

Disclosure; Figure 13; 57pp; German.

This invention describes a novel method for detecting microbial DNA/RNA
(I) by concentrating (I) from a sample, adding at least one labeled
oligonucleotide (ON), performing temperature-dependent hybridization and
determining (I) from the physical properties of the (I)-ON complex, e.g.
the temperature dependence of hybridization. The method is used for rapid
determination of microbial genomic RNA or DNA, particularly for diagnosis
of bacterial infections (e.g. sepsis) or fungal infections (particularly
in intensive care patients), also for monitoring food and water, and for
veterinary or forensic investigations. The method provides quick
determination/identification of microbial nucleic acid. It is very
sensitive, allowing early diagnosis of infection. AAH21160-AAH21231
represent primers and probes used to illustrate the method of the
invention.

Sequence 444 BP; 115 A; 89 C; 117 G; 118 T; 5 other;

Query Match 100.0%; Score 35; DB 22; Length 444;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTAGTCGCAATGTTATGTTAAGACTACGACG 35
395 CTAGTCGCAATGTTATGTTAAGACTACGACG 361

Search completed: August 6, 2003, 23:02:40
Job time : 219.75 secs

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OM nucleic - nucleic search, using sw model

Run on: August 6, 2003, 21:26:11 ; Search time 856.953 Seconds

(without alignments)
1670.846 Million cell updates/sec

Title: US-09-846-797-6

Perfect score: 35

Sequence: 1 ctactgcgcagtagttatggttaagactacgagc 35

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues 5777422

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_da:*
- 2: gb_hlg:*
- 3: gb_in:*
- 4: gb_cm:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
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- 11: gb_sts:*
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- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_or:*
- 21: em_ov:*
- 22: em_pat:*
- 23: em_ph:*
- 24: em_pl:*
- 25: em_ro:*
- 26: em_sts:*
- 27: em_un:*
- 28: em_vl:*
- 29: em_vt:*
- 30: em_hlg_hum:*
- 31: em_hlg_inv:*
- 32: em_hlg_other:*
- 33: em_hlg_pln:*
- 34: em_hlg_mus:*
- 35: em_hlg_rtd:*
- 36: em_hlg_mam:*
- 37: em_hlg_vrt:*
- 38: em_gy:*
- 39: em_hlgo_hum:*
- 40: em_hlgo_mus:*
- 41: em_hlgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	35	100.0	35 6 AX298064	AX298064 Sequence
2	35	100.0	51 6 AR107728	AR107728 Sequence
3	35	100.0	51 6 AR107732	AR107732 Sequence
4	35	100.0	52 6 AR107725	AR107725 Sequence
5	35	100.0	52 6 AR107726	AR107726 Sequence
6	35	100.0	52 6 AR107727	AR107727 Sequence
7	35	100.0	52 6 AR107730	AR107730 Sequence
8	35	100.0	72 8 LCU48426	UA8426 Linspora CO
9	35	100.0	75 6 AX406742	AX406742 Sequence
10	35	100.0	113 6 AX298065	AX298065 Sequence
11	35	100.0	113 6 AX298066	AX298066 Sequence
12	35	100.0	126 8 CA281374	Z81374 C. aeruginos
13	35	100.0	192 3 SARSSRB	M54960 S. gigantea
14	35	100.0	192 3 SARSSRB	X91535 Uncultured
15	35	100.0	261 3 S4172083	S41710 small subun
16	35	100.0	261 3 S4172652	S41713 small subun
17	35	100.0	266 8 EUSPUN4AB	Z69269 Uncultured
18	35	100.0	277 3 TOXRSS2	M17556 T. gondii sm
19	35	100.0	305 8 AF452625	AF452625 Glomus sp
20	35	100.0	311 8 AF213264	AF213264 Unculture
21	35	100.0	341 3 SN031148	U31148 Sarcocystis
22	35	100.0	346 8 AY150800	AY150800 Cladophila
23	35	100.0	346 8 MCUSUINB	AJ226070 Myrioscic
24	35	100.0	346 8 MCUSUINA	AJ226071 Myrioscic
25	35	100.0	347 8 MSCSSUNA	AJ226073 Myrioscic
26	35	100.0	347 8 MSCSSUNC	AJ226074 Myrioscic
27	35	100.0	347 8 MSCSSUND	AJ226075 Myrioscic
28	35	100.0	347 8 MSCSSUNE	AJ226076 Myrioscic
29	35	100.0	348 8 MDESSUINP	AJ226077 Myrioscic
30	35	100.0	364 3 AF424810	AF424810 Cryptospor
31	35	100.0	372 8 AY150799	AY150799 Cladophila
32	35	100.0	375 8 AY150798	AY150798 Cladophila
33	35	100.0	378 8 AF504732	AF504732 Unculture
34	35	100.0	379 8 AF504731	AF504731 Unculture
35	35	100.0	380 8 AF504734	AF504734 Unculture
36	35	100.0	381 8 AF247744	AF247744 Uncidentif
37	35	100.0	381 8 AF504733	AF504733 Unculture
38	35	100.0	382 8 AF504728	AF504728 Unculture
39	35	100.0	382 8 AF504729	AF504729 Unculture
40	35	100.0	384 8 EUSP51	Z69305 Uncultured
41	35	100.0	385 8 AF504735	AF504735 Unculture
42	35	100.0	390 3 AY029361	AY029361 Cryptospor
43	35	100.0	394 8 AY055059	AY055059 Ascomycot
44	35	100.0	402 8 AF183384	AF183384 Unculture
45	35	100.0	402 8 AY055060	AY055060 Ascomycot

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE
AX298064	AX298064	Sequence 6 from Patent WO0183821.	AX298064	AX298064.1	GI:17128150		Candida albicans	1	Hogan, J. J. and Gordon, P. C.	Polynucleotide probes for detection and quantitation of Candida species
							Candida albicans			
							Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
							Saccharomycetales; mitosporic Saccharomycetales; Candida.			

JOURNAL Patent: WO 0183821-A 6 08-NOV-2001;
Gen-Probe Incorporated (US)
FEATURES
source
1. 35
/organism="Candida albicans"
/mol_type="genomic DNA"
/db_xref="taxon:5476"
BASE COUNT 9 a 6 c 10 g 10 t
ORIGIN

Query Match 100.0%; Score 35; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTAGTCGCGCATAGTTTATGTTAGACTACGACGG 35
Db 1 CTAGTCGCGCATAGTTTATGTTAGACTACGACGG 35

RESULT 2
LOCUS AR107728/c 51 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 81 from patent US 6110665.
ACCESSION AR107728
VERSION AR107728.1 GI:12823215
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 51)
AUTHORS Fengler,C.K., Granstrom,D.E., Gajadhar,A.A. and Dubey,J.P.
TITLE Sarcocystis neuronadignostic primer and its use in methods of equine protozoal myeloencephalitis diagnosis
JOURNAL Patent: US 6110665-A 81 29-AUG-2000;
FEATURES location/Qualifiers
source 1. 51

BASE COUNT 17 a 12 c 11 g 11 t
ORIGIN

Query Match 100.0%; Score 35; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTAGTCGCGCATAGTTTATGTTAGACTACGACGG 35
Db 49 CTAGTCGCGCATAGTTTATGTTAGACTACGACGG 15

RESULT 3
LOCUS AR107732/c 51 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 85 from patent US 6110665.
ACCESSION AR107732
VERSION AR107732.1 GI:12823219
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 51)
AUTHORS Fengler,C.K., Granstrom,D.E., Gajadhar,A.A. and Dubey,J.P.
TITLE Sarcocystis neuronadignostic primer and its use in methods of equine protozoal myeloencephalitis diagnosis
JOURNAL Patent: US 6110665-A 85 29-AUG-2000;
FEATURES location/Qualifiers
source 1. 51

BASE COUNT 17 a 12 c 11 g 11 t
ORIGIN

Query Match 100.0%; Score 35; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTAGTCGCGCATAGTTTATGTTAGACTACGACGG 35
Db 49 CTAGTCGCGCATAGTTTATGTTAGACTACGACGG 15

RESULT 4
LOCUS AR107725/c 52 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 78 from patent US 6110665.
ACCESSION AR107725
VERSION AR107725.1 GI:12823212
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 52)
AUTHORS Fengler,C.K., Granstrom,D.E., Gajadhar,A.A. and Dubey,J.P.
TITLE Sarcocystis neuronadignostic primer and its use in methods of equine protozoal myeloencephalitis diagnosis
JOURNAL Patent: US 6110665-A 78 29-AUG-2000;
FEATURES location/Qualifiers
source 1. 52

BASE COUNT 18 a 12 c 11 g 11 t
ORIGIN

Query Match 100.0%; Score 35; DB 6; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTAGTCGCGCATAGTTTATGTTAGACTACGACGG 35
Db 50 CTAGTCGCGCATAGTTTATGTTAGACTACGACGG 16

RESULT 5
LOCUS AR107726/c 52 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 79 from patent US 6110665.
ACCESSION AR107726
VERSION AR107726.1 GI:12823213
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 52)
AUTHORS Fengler,C.K., Granstrom,D.E., Gajadhar,A.A. and Dubey,J.P.
TITLE Sarcocystis neuronadignostic primer and its use in methods of equine protozoal myeloencephalitis diagnosis
JOURNAL Patent: US 6110665-A 79 29-AUG-2000;
FEATURES location/Qualifiers
source 1. 52

BASE COUNT 18 a 12 c 11 g 11 t
ORIGIN

Query Match 100.0%; Score 35; DB 6; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTAGTCGCGCATAGTTTATGTTAGACTACGACGG 35
Db 50 CTAGTCGCGCATAGTTTATGTTAGACTACGACGG 16

RESULT 6
LOCUS AR107727/c 52 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 80 from patent US 6110665.
ACCESSION AR107727
VERSION AR107727.1 GI:12823214
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 52)
TITLE Fenger, C.K., Granstrom, D.E., Gajadhar, A.A. and Dubey, J.P.
JOURNAL Sarcocystis neurodiagnostic primer and its use in methods of
FEATURES equine protozoal myeloencephalitis diagnosis
Patent: US 6110665-A 80 29-AUG-2000;
Location/Qualifiers
Source 1..52
BASE COUNT 17 a 12 c 11 g 11 t 1 others
ORIGIN

Query Match 100.0%; Score 35; DB 6; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CTAGTCGGCATAGTTATGTTAAGACTACGACG 35
50 CTAGTCGGCATAGTTATGTTAAGACTACGACG 16

RESULT 7
LOCUS AR107730 52 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 83 from patent US 6110665.
ACCESSION AR107730
VERSION AR107730.1 GI:12823217
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 52)
AUTHORS Fenger, C.K., Granstrom, D.E., Gajadhar, A.A. and Dubey, J.P.
TITLE Sarcocystis neurodiagnostic primer and its use in methods of
JOURNAL equine protozoal myeloencephalitis diagnosis
FEATURES Patent: US 6110665-A 83 29-AUG-2000;
Location/Qualifiers
Source 1..52
BASE COUNT 18 a 12 c 11 g 11 t
ORIGIN

Query Match 100.0%; Score 35; DB 6; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CTAGTCGGCATAGTTATGTTAAGACTACGACG 35
50 CTAGTCGGCATAGTTATGTTAAGACTACGACG 16

RESULT 8
LOCUS LCU48426 72 bp DNA linear PLN 29-JUN-1996
DEFINITION Lanspora coronata nuclear-encoded small subunit ribosomal RNA gene,
ACCESSION U48426
VERSION U48426.1 GI:1399168
KEYWORDS
SOURCE Lanspora coronata
ORGANISM Lanspora coronata
REFERENCE Hypocremyces; Ascomycota; Pezizomycotina; Sordariomycetes;
AUTHORS Eukaryota; Fungi; Halosphaeriales; Halosphaeriaceae; Lanspora.
TITLE Spatafora, J.W., Volkman-Kohlmeier, B. and Kohlmeier, J.
JOURNAL Independent terrestrial origins of the Halosphaeriales (marine
REFERENCE Ascomycota)
AUTHORS unpublished
TITLE 2 (bases 1 to 72)
Spatafora, J.W., Volkman-Kohlmeier, B. and Kohlmeier, J.
Direct Submission

JOURNAL Submitted (02-FEB-1996) Joseph W. Spatafora, Botany & Plant
PATHOLOGY, Oregon State University, 2082 Cordley Hall, Corvallis,
OR 97331-2902, USA
FEATURES Location/Qualifiers
SOURCE 1..72
/organism="Lanspora coronata"
/mol_type="genomic DNA"
/strain="JK 4839A"
/db_xref="taxon:45830"
/note="from the culture collection of Jan and Brigitte
Kohlmeier (JK 4839A); amplified with primers NS1/NS4
(White et al., 1990) and sequenced with primers NS1, NS2,
NS4 (White et al., 1990), SR1R (Spatafora et al., 1995)
and SR7R (Vilgalys unpub.)."
complement(1..>72)
/product="small subunit ribosomal RNA"
BASE COUNT 18 a 16 c 15 g 23 t
ORIGIN

Query Match 100.0%; Score 35; DB 8; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CTAGTCGGCATAGTTATGTTAAGACTACGACG 35
41 CTAGTCGGCATAGTTATGTTAAGACTACGACG 7

RESULT 9
LOCUS AX406742 75 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 6 from Patent WO0227021.
ACCESSION AX406742
VERSION AX406742.1 GI:21439667
KEYWORDS
SOURCE Candida albicans
ORGANISM Candida albicans
REFERENCE Boettger, E.C., Rosenau, J., Kirschner, P. and Jack, T.
AUTHORS Method for detecting fungal infections
TITLE Patent: WO 0227021-A 6 04-APR-2002;
JOURNAL Cytomet GmbH & Co. KG (DE)
FEATURES Location/Qualifiers
SOURCE 1..75
/organism="Candida albicans"
/mol_type="genomic DNA"
/db_xref="taxon:5476"
BASE COUNT 15 a 20 c 14 g 25 t 1 others
ORIGIN

Query Match 100.0%; Score 35; DB 6; Length 75;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CTAGTCGGCATAGTTATGTTAAGACTACGACG 35
8 CTAGTCGGCATAGTTATGTTAAGACTACGACG 42

RESULT 10
LOCUS AX298065 113 bp DNA linear PAT 26-NOV-2001
DEFINITION Sequence 7 from Patent WO0183821.
ACCESSION AX298065
VERSION AX298065.1 GI:17128151
KEYWORDS
SOURCE Candida albicans
ORGANISM Candida albicans
REFERENCE Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
TITLE Saccharomycetales; mitosporic Saccharomycetales; Candida.

AUTHORS Hogan, J.J. and Gordon, P.C.
 TITLE Polynucleotide probes for detection and quantitation of *Candida*
 JOURNAL Species
 Patent: WO 0183821-A 7 08-NOV-2001;
 Gen-Probe Incorporated (US)
 FEATURES Location/Qualifiers
 SOURCE 1..113
 /organism="Candida albicans"
 /mol_type="genomic DNA"
 /db_xref="taxon:5476"
 misc_structure 1..113
 /note="Probe domain"
 BASE COUNT 35 a 27 c 23 g 28 t
 ORIGIN
 Query Match 100.0%; Score 35; DB 6; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGTCGCATAGTTATGTTAAGACTACGACGG 35
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 70 CTAGTCGCATAGTTATGTTAAGACTACGACGG 104

Db

RESULT 11
 AX298066/c 113 bp mRNA linear PAT 26-NOV-2001
 LOCUS AX298066
 DEFINITION Sequence 8 from Patent WO0183821.
 ACCESSION AX298066
 VERSION AX298066.1 GI:17128152
 KEYWORDS
 SOURCE
 ORGANISM
 CANDIDA ALBICANS
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; mitosporic Saccharomycetales; Candida.

REFERENCE 1
 AUTHORS Hogan, J.J. and Gordon, P.C.
 TITLE Polynucleotide probes for detection and quantitation of *Candida*
 JOURNAL Species
 Patent: WO 0183821-A 8 08-NOV-2001;
 Gen-Probe Incorporated (US)
 FEATURES Location/Qualifiers
 SOURCE 1..113
 /organism="Candida albicans"
 /mol_type="mRNA"
 /db_xref="taxon:5476"
 misc_structure 1..113
 /note="Sequence of rRNA target region"
 BASE COUNT 28 a 23 c 27 g 35 t
 ORIGIN
 Query Match 100.0%; Score 35; DB 6; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGTCGCATAGTTATGTTAAGACTACGACGG 35
 |||
 44 CTAGTCGCATAGTTATGTTAAGACTACGACGG 10

Db

RESULT 12
 CAZ81374 126 bp DNA linear PLN 22-JAN-1998
 LOCUS CAZ81374
 DEFINITION C. aeruginosa 18S rRNA gene.
 ACCESSION Z81374
 VERSION Z81374.1 GI:2808818
 KEYWORDS 18S ribosomal RNA; 18S rRNA gene.
 SOURCE Chlorociboria aeruginosa
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
 Helotiales; Helotiaceae; Chlorociboria.
 REFERENCE 1 (bases 1 to 126)
 AUTHORS Holst-Jensen, A.

TITLE Direct Submission
 JOURNAL Submitted (29-OCT-1996) Holst-Jensen A., Division of Botany,
 Department of Biology, University of Oslo, P.O. Box 1045, Blindern
 0316, Oslo, NORWAY
 FEATURES Location/Qualifiers
 SOURCE 1..126
 /organism="Chlorociboria aeruginosa"
 /mol_type="genomic DNA"
 /strain="1785.P on dead hardwood"
 /db_xref="taxon:54693"
 gene 1..126
 /gene="18S rRNA"
 rRNA <1..>126
 /gene="18S rRNA"
 /product="18S ribosomal RNA"
 BASE COUNT 30 a 26 c 34 g 36 t
 ORIGIN
 Query Match 100.0%; Score 35; DB 8; Length 126;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGTCGCATAGTTATGTTAAGACTACGACGG 35
 |||
 41 CTAGTCGCATAGTTATGTTAAGACTACGACGG 7

Db

RESULT 13
 SARSSRB/c 192 bp rRNA linear INV 27-APR-1993
 LOCUS SARSSRB/c
 DEFINITION S.gigantea small subunit ribosomal RNA.
 ACCESSION M54960 M37052
 VERSION M54960.1 GI:175888
 KEYWORDS ribosomal RNA small subunit.
 SOURCE Sarcocystis gigantea
 ORGANISM SARCOCYSTIS GIGANTEA
 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 Sarcocystidae; Sarcocystis.

REFERENCE 1 (bases 1 to 192)
 AUTHORS Johnson, A.M., Iilana, S., Hakendorf, P. and Baverstock, P.R.
 TITLE Phylogenetic relationships of the apicomplexan protist *Sarcocystis*
 JOURNAL as determined by small subunit ribosomal RNA comparison
 MEDLINE J. Parasitol. 74 (5), 847-860 (1988)
 PUBMED 88332524
 COMMENT 3138398
 FEATURES Original source text: S.gigantea ribosomal RNA.
 SOURCE Location/Qualifiers
 1..192
 /organism="Sarcocystis gigantea"
 /mol_type="rRNA"
 /db_xref="taxon:5814"
 BASE COUNT 65 a 36 c 39 g 52 t
 ORIGIN
 Query Match 100.0%; Score 35; DB 3; Length 192;
 Best Local Similarity 100.0%; Pred. No. 0.93;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGTCGCATAGTTATGTTAAGACTACGACGG 35
 |||
 140 CTAGTCGCATAGTTATGTTAAGACTACGACGG 106

Db

RESULT 14
 ESPX91535/c 217 bp DNA linear PLN 10-FEB-2003
 LOCUS ESPX91535
 DEFINITION Uncultured saccharomycete partial 18S rRNA gene (clone group K20).
 ACCESSION X91535
 VERSION X91535.1 GI:987810
 KEYWORDS 18S ribosomal RNA; 18S rRNA gene.
 SOURCE uncultured saccharomycete
 ORGANISM uncultured saccharomycete
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

unclassified Saccharomycetes; environmental samples.

REFERENCE 1
AUTHORS Pedersen, K.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 217)
AUTHORS Pedersen, K.
JOURNAL Direct Submission
Submitted (13-SEP-1995) K. Pedersen, Lundberg Institute, General
and Marine Microbiology, Medicinaregatan 9 E, 413 90 Goeteborg,
SWEDEN

FEATURES
source
1. .217
location/Qualifiers

/organism="uncultured saccharomycete"
/mol_type="genomic DNA"
/isolation_source="Isolated from bentonite/sand buffer
material from the underground research laboratory at
AECL/Whiteshell laboratories"
/db_xref="taxon:212404"
/clone="clone group K20"
/environmental_sample
/country="Canada"
1. .217
/gene="18S rRNA"
<1. .>217
/gene="18S rRNA"
/product="18S ribosomal RNA"

BASE COUNT 65 a 36 c 55 g 61 t
ORIGIN

Query Match 100.0%; Score 35; DB 8; Length 217;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGTCGCATAGTTTATGTTAGACTACGACGG 35
|||||
DB 200 CTAGTCGCATAGTTTATGTTAGACTACGACGG 166

RESULT 15
S41720S3/C 261 bp RNA linear INV 08-MAY-1993
LOCUS
DEFINITION small subunit rRNA (D/A-region and B-region) [Sarcocystis
capracanis, rRNA Partial, 261 nt, segment 3 of 3].
ACCESSION S41710
VERSION S41710.1 GI:252752

SEGMENT 3 of 3
SOURCE Sarcocystis capracanis
ORGANISM Sarcocystis capracanis
Eukaryota; Alveolata; Apicomplexa; Coccidia; Elmeriida;
Sarcocystidae; Sarcocystis.

REFERENCE 1 (bases 1 to 261)
AUTHORS Tenier, A.M., Baverstock, P.R. and Johnson, A.M.
TITLE Phylogenetic relationships of Sarcocystis species from sheep,
goats, cattle and mice based on ribosomal RNA sequences
JOURNAL Int. J. Parasitol. 22 (4), 503-513 (1992)
MEDLINE 92355206
PUBMED 1644525

REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI g1dbsq 110244] from the original journal article.
This sequence comes from Fig. 1C and 1D.
location/Qualifiers

1. .261
/organism="Sarcocystis capracanis"
/mol_type="rRNA"
/db_xref="taxon:5816"

gene order(S41720.1:1..210,join(S41716.1:1..61,1..261))
rRNA order(S41720.1:1..210,join(S41716.1:1..61,1..261))
/gene="small subunit rRNA"
/product="small subunit rRNA"

BASE COUNT 77 a 43 c 53 g 70 t 18 others
ORIGIN

Query Match 100.0%; Score 35; DB 3; Length 261;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGTCGCATAGTTTATGTTAGACTACGACGG 35
|||||
DB 202 CTAGTCGCATAGTTTATGTTAGACTACGACGG 168

Search completed: August 6, 2003, 23:29:02
Job time : 858.953 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using SW model

Run on: August 6, 2003, 22:51:21 / Search time 1568.72 seconds
(without alignments)
449.303 Million cell updates/sec

Title: US-09-846-797-1

Perfect score: 29

Sequence: 1 ggcgcataaagaacacacacgaccc 29

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 segs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

EST:
1: em_estdb:
2: em_esthum:
3: em_estin:
4: em_estnu:
5: em_estor:
6: em_estpl:
7: em_estro:
8: em_estc:
9: gb_estl:
10: gb_estc:
11: gb_esth:
12: gb_estj:
13: gb_estd:
14: gb_estf:
15: em_estfun:
16: em_estom:
17: em_gss_hum:
18: em_gss_inu:
19: em_gss_pln:
20: em_gss_vit:
21: em_gss_fun:
22: em_gss_mam:
23: em_gss_mus:
24: em_gss_pro:
25: em_gss_rtd:
26: em_gss_pbg:
27: em_gss_vrl:
28: gb_gssl:
29: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	29	100.0	615	10	BE337371 894045E04
C 2	29	100.0	943	29	AL439313 T7 end of
C 3	29	100.0	949	29	AL440561 T3 end of
C 4	29	100.0	959	29	AL441487 T7 end of

C 5	29	100.0	961	29	CNS07DW1	AL440999 T7 end of
C 6	29	100.0	966	29	CNS07E4J	AL441305 T7 end of
C 7	29	100.0	971	29	CNS07DAJ	AL442225 T7 end of
C 8	29	100.0	994	29	CNS07CJ3	AL438633 T7 end of
C 9	29	100.0	996	29	CNS07CJX	AL438915 T7 end of
C 10	29	100.0	1010	29	CNS07CCK	AL439015 T7 end of
C 11	29	100.0	1027	29	CNS07CRE	AL439536 T3 end of
C 12	29	100.0	1029	29	CNS07E90	AL441469 T3 end of
C 13	29	100.0	1036	29	CNS07DKX	AL440599 T7 end of
C 14	29	100.0	1038	29	CNS07DH7	AL440465 T7 end of
C 15	29	100.0	1038	29	CNS07C9I	AL438892 T7 end of
C 16	29	100.0	1041	29	CNS07CNA	AL438892 T7 end of
C 17	29	100.0	1066	29	CNS07DIY	AL439388 T3 end of
C 18	29	100.0	1071	29	CNS07E4H	AL439916 T3 end of
C 19	29	100.0	1120	29	CNS07EC4	AL441519 T7 end of
C 20	29	98.6	980	29	CNS07CEX	AL441578 T3 end of
C 21	29	94.5	997	29	CNS07DD1	AL438087 T7 end of
C 22	29	89.0	888	29	CNS06VOP	AL440783 T7 end of
C 23	29	89.0	889	29	CNS06W2D	AL417623 T3 end of
C 24	29	89.0	928	29	CNS06V38	AL419087 T3 end of
C 25	29	89.0	934	29	CNS06VMT	AL416634 T7 end of
C 26	29	89.0	941	29	CNS06X3M	AL417564 T3 end of
C 27	29	89.0	944	29	CNS06X1I	AL419240 T7 end of
C 28	29	89.0	949	29	CNS07B5Y	AL419164 T7 end of
C 29	29	89.0	958	29	CNS06BEM	AL437468 T7 end of
C 30	29	89.0	1034	29	CNS07AS1	AL418232 T3 end of
C 31	29	87.6	1077	29	CNS07B2A	AL436984 T7 end of
C 32	29	85.5	906	29	CNS06X2U	AL437336 T3 end of
C 33	29	85.5	809	29	CNS06XUP	AL419680 T3 end of
C 34	29	85.5	927	29	CNS07A54	AL418523 T3 end of
C 35	29	80.0	854	13	BUI80498	AL436142 T7 end of
C 36	29	77.9	502	29	B2301816	AL436142 T7 end of
C 37	29	75.2	710	29	CNS07BRJ	B2301816 K01489.q1
C 38	29	72.4	224	28	A2931573	B2305052 K03296.p1
C 39	29	72.4	292	28	A2124549	AL438245 T7 end of
C 40	29	72.4	381	28	A2931738	A2931573 474.dh286
C 41	29	72.4	438	28	A2929878	A2124549 b107r.S.
C 42	29	72.4	440	28	A2930332	A2931738 474.dh289
C 43	29	72.4	459	29	CNS06XPK	A2929878 479.d1156
C 44	29	72.4	467	28	A2929872	A2930332 474.dh253
C 45	29	72.4	473	29	CNS06XTD	AL420174 T3 end of
						A2929872 479.d1156
						AL420167 T7 end of

ALIGNMENTS

RESULT 1
BE337371 615 bp mRNA linear EST 14-Jul-2000
LOCUS 894045E04.x1 C. reinhardtii CC-1690, normalized, Lambda zap II
DEFINITION Chlamydomonas reinhardtii cDNA, mRNA sequence.

ACCESSION BE337371
VERSION BE337371.1 GI:9210456
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii

REFERENCE Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P.,
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.

AUTHORS Modermott, J. P., Sillflow, C., Stern, D. and Surryck, R.
TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model,
JOURNAL Unicellular System for Analyzing Gene Function and Regulation in
COMMENT Unpublished
CONTACT: Elizabeth H. Harris
DCMB Box 91000
Duke University,
Durham, NC 27708-1000, USA
Tel: 919 613 8164
Fax: 919 613 8177
Email: chlamy@duke.edu.
Location/Qualifiers

FEATURES

source

1. .615
 /organism="Chlamydomonas reinhardtii"
 /mol_type="mRNA"
 /strain="CC-1690 wild type mt+ 21gr"
 /db_xref="taxon:3055"
 /clone_11b="C. reinhardtii CC-1690, normalized, Lambda Zap II"
 /note="Vector: Bluescript II SK-, Site.1: EcoRI; Site.2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in YAP (acetate-containing) medium in the light, YAP medium in the dark, HS (minimal) medium in ambient levels of CO₂ and HS medium bubbled with 5% CO₂. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into Lambda Zap II (Stratagene) in the EcoRI (5') and XhoI (3') sites. Bluescript II SK- plasmids were excised from the lambda Zap clones by superinfection with Exsist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."

BASE COUNT 169 a 104 c 163 g 179 t
 ORIGIN

Query Match 100.0%; Score 29; DB 10; Length 615;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTCAATTAAGACACACACCGATCCC 29
 ||||||||||||||||||||||||||||
 Db 277 GCCTCAATTAAGACACACACCGATCCC 249

RESULT 2
 CENS07CL7/c 943 bp DNA linear GSS 08-JUL-2001
 LOCUS
 DEFINITION T7 end of clone BD0AA003G09 of library BD0A from strain CBS 94 of
 Candida tropicalis, genomic survey sequence.
 AL439313
 AL439313.1 GI:12222726
 GSS.
 SOURCE
 ORGANISM
 Candida tropicalis
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; mitosporic Saccharomycetales; Candida.
 1 (bases 1 to 943)
 Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
 Bolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
 de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
 Malpertuy,A., Neugeglise,C., Ozler-Kalogeropoulos,O., Potter,S.,
 Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
 Wincker,P. and Weissenbach,J.
 Genomic exploration of the hemiascomycetous yeasts: 1. A set of
 yeast species for molecular evolution studies

JOURNAL
 MEDLINE
 PUBMED
 FEBS Lett. 487 (1), 3-12 (2000)
 20584711
 11152876

REFERENCE
 AUTHORS
 Blandin,G., Ozler-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
 Dujon,B.

TITLE
 Genomic exploration of the hemiascomycetous yeasts: 16. Candida
 tropicalis
 JOURNAL
 MEDLINE
 PUBMED
 FEBS Lett. 487 (1), 91-94 (2000)
 20584726
 11152891
 3 (bases 1 to 943)
 Genoscope.
 Direct Submission
 Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
 seqref@genoscope.cns.fr - Web :
 This GSS is part of a random genomic sequencing program of thirteen
 yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
 exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,

COMMENT

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
 lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
 angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
 Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
 5 kb were prepared and both extremities were sequenced. See
 keywords for description of this sequence and for the sequence of
 the other extremity of this insert.

FEATURES

source

1. .943
 /organism="Candida tropicalis"
 /mol_type="genomic DNA"
 /strain="CBS 94"
 /db_xref="taxon:5482"
 /clone="BD0AA003G09"
 /clone_11b="BD0AA"
 /note="end : T7"
 <1. >943
 /note="part of rDNA repeats
 contains 35S rDNA"
 /evidence=not_experimental

BASE COUNT 249 a 173 c 242 g 269 t
 ORIGIN

Query Match 100.0%; Score 29; DB 29; Length 943;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTCAATTAAGACACACACCGATCCC 29
 ||||||||||||||||||||||||||||
 Db 597 GCCTCAATTAAGACACACACCGATCCC 569

RESULT 3
 CENS07DJV/c 949 bp DNA linear GSS 08-JUL-2001
 LOCUS
 DEFINITION T3 end of clone BD0AA013C01 of library BD0A from strain CBS 94 of
 Candida tropicalis, genomic survey sequence.
 AL440561
 AL440561.1 GI:12223972
 GSS.
 SOURCE
 ORGANISM
 Candida tropicalis
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; mitosporic Saccharomycetales; Candida.
 1 (bases 1 to 949)
 Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
 Bolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
 de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
 Malpertuy,A., Neugeglise,C., Ozler-Kalogeropoulos,O., Potter,S.,
 Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
 Wincker,P. and Weissenbach,J.
 Genomic exploration of the hemiascomycetous yeasts: 1. A set of
 yeast species for molecular evolution studies

JOURNAL
 MEDLINE
 PUBMED
 FEBS Lett. 487 (1), 3-12 (2000)
 20584711
 11152876

REFERENCE
 AUTHORS
 Blandin,G., Ozler-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
 Dujon,B.

TITLE
 Genomic exploration of the hemiascomycetous yeasts: 16. Candida
 tropicalis
 JOURNAL
 MEDLINE
 PUBMED
 FEBS Lett. 487 (1), 91-94 (2000)
 20584726
 11152891
 3 (bases 1 to 949)
 Genoscope.
 Direct Submission
 Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
 seqref@genoscope.cns.fr - Web :
 This GSS is part of a random genomic sequencing program of thirteen
 yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
 exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,

COMMENT

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

Location/Qualifiers

1..949
/organism="Candida tropicalis"
/mol_type="genomic DNA"
/strain="CBS 94"
/db_xref="taxon:5482"
/clone="BD0AA013C01"
/clone_11b="BD0AA"
/note="end : T3"
<1..>949
/note="part of rDNA repeats
contains 35S rDNA"
/evidence=not_experimental

misc.feature

BASE COUNT 251 a 179 c 260 g 253 t 6 others
ORIGIN

Query Match 100.0%; Score 29; DB 29; Length 949;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTCATTAAGAACACACACCGATCCC 29
Db 213 GCCTCATTAAGAACACACACCGATCCC 185

RESULT 4
LOCUS CNS07E9L 959 bp DNA linear GSS 08-JUL-2001
DEFINITION T7 end of clone XBD0AA002C12 of library XBD0AA from strain CBS 94
ACCESSION AL441487
VERSION AL441487.1 GI:12224713
KEYWORDS GSS.
SOURCE Candida tropicalis
ORGANISM Candida tropicalis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
1 (bases 1 to 959)
Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Boloetin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Florente,B.,
Malpertuy,A., Neveuglise,C., Ozler-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.

REFERENCE
AUTHORS
TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
PUBMED 11152876
2 (bases 1 to 959)
Blandin,G., Ozler-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
Dujon,B.

TITLE Genomic exploration of the hemiascomycetous yeasts: 16. Candida
tropicalis
JOURNAL FEBS Lett. 487 (1), 91-94 (2000)
MEDLINE 20584726
PUBMED 11152891
3 (bases 1 to 959)
Genoscope.
AUTHORS
REFERENCE
TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequenage,
2 rue Gaston Cremlieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segre@genoscope.cns.fr Web :
http://www.genoscope.cns.fr)

COMMENT This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii.

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

Location/Qualifiers

1..959
/organism="Candida tropicalis"
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/note="end : T7"
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/note="part of rDNA repeats
contains 18S rDNA"
/evidence=not_experimental

misc.feature

BASE COUNT 267 a 188 c 249 g 252 t 3 others
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Query Match 100.0%; Score 29; DB 29; Length 959;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTCATTAAGAACACACACCGATCCC 29
Db 794 GCCTCATTAAGAACACACACCGATCCC 766

RESULT 5
LOCUS CNS07DW1L 961 bp DNA linear GSS 08-JUL-2001
DEFINITION T7 end of clone BD0AA016B05 of library BD0AA from strain CBS 94 of
Candida tropicalis, genomic survey sequence.
ACCESSION AL440999
VERSION AL440999.1 GI:12224407
KEYWORDS GSS.
SOURCE Candida tropicalis
ORGANISM Candida tropicalis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
1 (bases 1 to 961)
Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Boloetin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Florente,B.,
Malpertuy,A., Neveuglise,C., Ozler-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.

REFERENCE
AUTHORS
TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
PUBMED 11152876
2 (bases 1 to 961)
Blandin,G., Ozler-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
Dujon,B.

TITLE Genomic exploration of the hemiascomycetous yeasts: 16. Candida
tropicalis
JOURNAL FEBS Lett. 487 (1), 91-94 (2000)
MEDLINE 20584726
PUBMED 11152891
3 (bases 1 to 961)
Genoscope.
AUTHORS
REFERENCE
TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequenage,
2 rue Gaston Cremlieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segre@genoscope.cns.fr Web :
http://www.genoscope.cns.fr)

COMMENT This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii.

Saccharomyces kluyveri, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

SOURCE

1..961
/organism="Candida tropicalis"
/mol_type="genomic DNA"
/strain="CBS 94"
/db_xref="taxon:5482"
/clone="BD0A016B05"
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/note="end : T7"
<1..>961
/note="part of rDNA repeats
contains 35S rDNA"
/evidence="not_experimental"

misc_feature

BASE COUNT 252 a 182 c 256 g 268 t 3 others
ORIGIN

Query Match 100.0%; Score 29; DB 29; Length 961;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCGTCATTAAGACACACACCGATCCC 29
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Db 502 GCGTCATTAAGACACACACCGATCCC 474

RESULT 6
CNS07E4J/c 966 bp DNA linear GSS 08-JUL-2001
LOCUS
DEFINITION T7 end of clone XBD0A01A07 of library XBD0A from strain CBS 94
ACCESSION AL441305
VERSION AL441305.1 GI:12224531
KEYWORDS
SOURCE GSS.
ORGANISM *Candida tropicalis*
Candida tropicalis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.

REFERENCE
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neugeilise,C., Ozler-Kalogeropoulos,O., Potter,S.,
Saurin,M., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.

TITLE
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584726
PUBMED 11152876

REFERENCE
AUTHORS Blandin,G., Ozler-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
Dujon,B.

TITLE
JOURNAL FEBS Lett. 487 (1), 91-94 (2000)
MEDLINE 20584726
PUBMED 11152891
REFERENCE 3 (bases 1 to 966)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segref@genoscope.cns.fr - Web :
This GSS is part of a random genomic sequencing program of thirteen
yeast species: *Saccharomyces bayanus* var. *uvaurum*, *Saccharomyces*
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Saccharomyces kluyveri, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

SOURCE

1..966
/organism="Candida tropicalis"
/mol_type="genomic DNA"
/strain="CBS 94"
/db_xref="taxon:5482"
/clone="XBD0A01A07"
/clone_1lb="XBD0A"
/note="end : T7"
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/note="part of rDNA repeats
contains 35S rDNA"
/evidence="not_experimental"

misc_feature

BASE COUNT 243 a 190 c 240 g 274 t 19 others
ORIGIN

Query Match 100.0%; Score 29; DB 29; Length 966;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCGTCATTAAGACACACACCGATCCC 29
|||||
Db 85 GCGTCATTAAGACACACACCGATCCC 57

RESULT 7
CNS07DAJ/c 971 bp DNA linear GSS 08-JUL-2001
LOCUS
DEFINITION T7 end of clone BD0A010H04 of library BD0A from strain CBS 94 of
Candida tropicalis, genomic survey sequence.
ACCESSION AL440225
VERSION AL440225.1 GI:12223636
KEYWORDS
SOURCE GSS.
ORGANISM *Candida tropicalis*
Candida tropicalis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.

REFERENCE
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neugeilise,C., Ozler-Kalogeropoulos,O., Potter,S.,
Saurin,M., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.

TITLE
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584726
PUBMED 11152876

REFERENCE
AUTHORS Blandin,G., Ozler-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
Dujon,B.

TITLE
JOURNAL FEBS Lett. 487 (1), 91-94 (2000)
MEDLINE 20584726
PUBMED 11152891
REFERENCE 3 (bases 1 to 971)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segref@genoscope.cns.fr - Web :
This GSS is part of a random genomic sequencing program of thirteen
yeast species: *Saccharomyces bayanus* var. *uvaurum*, *Saccharomyces*
exiguus, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*.

COMMENT

COMMENT

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

SOURCE

1..971
/organism="Candida tropicalis"
/mol_type="genomic DNA"
/strain="CBS 94"
/db_xref="taxon:5482"
/clone="BD0A010H04"
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/note="end : 77"
<1..>971
/note="part of rDNA repeats
contains 35S rDNA"
/evidence="not-experimental"

misc_feature

BASE COUNT 253 a 188 c 252 g 272 t 6 others
ORIGIN

Query Match 100.0%; Score 29; DB 29; Length 971;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGTCATTAAGACACACACCGATCCC 29
Db 374 GCGTCATTAAGACACACACCGATCCC 346

RESULT 8
LOCUS CNS07CU3 994 bp DNA linear GSS 08-JUL-2001
DEFINITION T7 end of clone BD0A006H01 of library BD0A from strain CBS 94 of
ACCESSION AL439633
VERSION AL439633.1 GI:12223046
KEYWORDS GSS.
SOURCE Candida tropicalis
ORGANISM Candida tropicalis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.

REFERENCE
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
1 (bases 1 to 994)
Bolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvéglise,C., Ozler-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
JOURNAL yeast species for molecular evolution studies
MEDLINE FEBS Lett. 487 (1), 3-12 (2000)
PUBMED 20584711
11152876

REFERENCE
AUTHORS Blandin,G., Ozler-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
Dujon,B.

TITLE Genomic exploration of the hemiascomycetous yeasts: 16. Candida
JOURNAL tropicalis
MEDLINE FEBS Lett. 487 (1), 91-94 (2000)
PUBMED 20584726
11152891

REFERENCE
AUTHORS 3 (bases 1 to 994)
Genoscope.

TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequençage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segref@genoscope.cns.fr - Web :
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii.

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

SOURCE

1..994
/organism="Candida tropicalis"
/mol_type="genomic DNA"
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/db_xref="taxon:5482"
/clone="BD0A006H01"
/clone_1lb="BD0AA"
/note="end : 77"
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/note="part of rDNA repeats
contains 35S rDNA"
/evidence="not-experimental"

misc_feature

BASE COUNT 283 a 263 c 189 g 258 t 1 others
ORIGIN

Query Match 100.0%; Score 29; DB 29; Length 994;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGTCATTAAGACACACACCGATCCC 29
Db 502 GCGTCATTAAGACACACACCGATCCC 530

RESULT 9
LOCUS CNS07CCX 996 bp DNA linear GSS 08-JUL-2001
DEFINITION T7 end of clone BD0A001H09 of library BD0A from strain CBS 94 of
ACCESSION AL439015
VERSION AL439015.1 GI:12222428
KEYWORDS GSS.
SOURCE Candida tropicalis
ORGANISM Candida tropicalis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.

REFERENCE
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
1 (bases 1 to 996)
Bolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvéglise,C., Ozler-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
JOURNAL yeast species for molecular evolution studies
MEDLINE FEBS Lett. 487 (1), 3-12 (2000)
PUBMED 20584711
11152876

REFERENCE
AUTHORS Blandin,G., Ozler-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
Dujon,B.

TITLE Genomic exploration of the hemiascomycetous yeasts: 16. Candida
JOURNAL tropicalis
MEDLINE FEBS Lett. 487 (1), 91-94 (2000)
PUBMED 20584726
11152891

REFERENCE
AUTHORS 3 (bases 1 to 996)
Genoscope.

TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequençage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segref@genoscope.cns.fr - Web :
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii.

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

source

1..996
/organism="Candida tropicalis"
/mol_type="genomic DNA"
/strain="CBS 94"
/db_xref="taxon:5482"
/clone="BD0A001H09"
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/note="end : T7"
<1..>996

misc_feature

/note="part of rDNA repeats
contains 18S rDNA"
/evidence="not-experimental"

BASE COUNT 268 a 256 c 192 g 278 t 2 others
ORIGIN

Query Match 100.0%; Score 29; DB 29; Length 996;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTCATTAAGAACACACCGATCCC 29
Db 191 GCCTCATTAAGAACACACCGATCCC 219

RESULT 10
CNS07CRE/LOCUS
DEFINITION T3 end of clone BD0A006B09 of library BD0AA from strain CBS 94 of
ACCESSION AL439536
VERSION AL439536.1 GI:12222949
KEYWORDS GSS.
SOURCE Candida tropicalis
ORGANISM Candida tropicalis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.

REFERENCE 1 (bases 1 to 1010)
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Lorente,B.,
Malpertuy,A., Neuvéglise,C., Ozler-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
PUBMED 11152876

REFERENCE 2 (bases 1 to 1010)
AUTHORS Blandin,G., Ozler-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
Dujon,B.

TITLE Genomic exploration of the hemiascomycetous yeasts: 16. Candida
tropicalis
JOURNAL FEBS Lett. 487 (1), 91-94 (2000)
MEDLINE 20584726
PUBMED 11152891
REFERENCE 3 (bases 1 to 1010)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segref@genoscope.cns.fr - Web :
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Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

source

1..1010
/organism="Candida tropicalis"
/mol_type="genomic DNA"
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/db_xref="taxon:5482"
/clone="BD0A006B09"
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/note="end : T3"
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misc_feature

/note="part of rDNA repeats
contains 35S rDNA"
/evidence="not-experimental"

BASE COUNT 266 a , 201 c 258 g 284 t 1 others
ORIGIN

Query Match 100.0%; Score 29; DB 29; Length 1010;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTCATTAAGAACACACCGATCCC 29
Db 38 GCCTCATTAAGAACACACCGATCCC 10

RESULT 11
CNS07E90/LOCUS
DEFINITION T3 end of clone XBD0A002C01 of library XBD0A from strain CBS 94
ACCESSION AL441466
VERSION AL441466.1 GI:12224692
KEYWORDS GSS.
SOURCE Candida tropicalis
ORGANISM Candida tropicalis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.

REFERENCE 1 (bases 1 to 1027)
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Lorente,B.,
Malpertuy,A., Neuvéglise,C., Ozler-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
PUBMED 11152876

REFERENCE 2 (bases 1 to 1027)
AUTHORS Blandin,G., Ozler-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
Dujon,B.

TITLE Genomic exploration of the hemiascomycetous yeasts: 16. Candida
tropicalis
JOURNAL FEBS Lett. 487 (1), 91-94 (2000)
MEDLINE 20584726
PUBMED 11152891
REFERENCE 3 (bases 1 to 1027)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segref@genoscope.cns.fr - Web :
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COMMENT

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FEATURES

source

1..1027
/organism="Candida tropicalis"
/mol_type="genomic DNA"
/strain="CBS 94"
/db_xref="taxon:5482"
/clone="XBD0A002C01"
/clone_1lb="XBD0A"
/note="end : T3"
<1..>1027
/note="part of rDNA repeats
contains 18S rDNA"
/evidence="not_experimental"

misc_feature

BASE COUNT 287 a 195 c 264 g 279 t 2 others
ORIGIN

Query Match 100.0%; Score 29; DB 29; Length 1027;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTCAATAAAGACACACCGATCCC 29
Db 879 GCGTCATAATAAGACACACCGATCCC 851

RESULT 12
CNS07DKX/c 1029 bp DNA linear GSS 08-JUL-2001
LOCUS T7 end of clone BD0A013E02 of library BD0A from strain CBS 94 of
DEFINITION Candida tropicalis, genomic survey sequence.
ACCESSION AL440599
VERSION AL440599.1 GI:12224010
KEYWORDS GSS.
SOURCE Candida tropicalis
ORGANISM Candida tropicalis

REFERENCE
AUTHORS Souciet,J.L., Algbe,M., Artiguenave,F., Blandin,G.,
1 (bases 1 to 1029)
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvéglise,C., Ozler-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
JOURNAL yeast species for molecular evolution studies
MEDLINE FEBS Lett. 487 (1), 3-12 (2000)
PUBMED 20584711

REFERENCE
AUTHORS Blandin,G., Ozler-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
Dujon,B.

TITLE Genomic exploration of the hemiascomycetous yeasts: 16. Candida
JOURNAL tropicalis
MEDLINE FEBS Lett. 487 (1), 91-94 (2000)
PUBMED 20584726

REFERENCE
AUTHORS 3 (bases 1 to 1029)
Genoscope.

TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segre@genoscope.cns.fr - Web :
JOURNAL This GSS is part of a random genomic sequencing program of thirteen
COMMENT yeast species: *Saccharomyces bayanus* var. *uvatum*, *Saccharomyces*
exiguus, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*,

Saccharomyces kluyveri, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

source

1..1029
/organism="Candida tropicalis"
/mol_type="genomic DNA"
/strain="CBS 94"
/db_xref="taxon:5482"
/clone="BD0A013E02"
/clone_1lb="BD0A"
/note="end : T7"
<1..>1029
/note="part of rDNA repeats
contains 35S rDNA"
/evidence="not_experimental"

misc_feature

BASE COUNT 261 a 216 c 272 g 277 t 3 others
ORIGIN

Query Match 100.0%; Score 29; DB 29; Length 1029;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTCAATAAAGACACACCGATCCC 29
Db 111 GCGTCATAATAAGACACACCGATCCC 83

RESULT 13
CNS07DH7/c 1036 bp DNA linear GSS 08-JUL-2001
LOCUS T7 end of clone BD0A012F03 of library BD0A from strain CBS 94 of
DEFINITION Candida tropicalis, genomic survey sequence.
ACCESSION AL440465
VERSION AL440465.1 GI:12223876
KEYWORDS GSS.
SOURCE Candida tropicalis
ORGANISM Candida tropicalis

REFERENCE
AUTHORS Souciet,J.L., Algbe,M., Artiguenave,F., Blandin,G.,
1 (bases 1 to 1036)
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvéglise,C., Ozler-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
JOURNAL yeast species for molecular evolution studies
MEDLINE FEBS Lett. 487 (1), 3-12 (2000)
PUBMED 20584711

REFERENCE
AUTHORS Blandin,G., Ozler-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
Dujon,B.

TITLE Genomic exploration of the hemiascomycetous yeasts: 16. Candida
JOURNAL tropicalis
MEDLINE FEBS Lett. 487 (1), 91-94 (2000)
PUBMED 20584726

REFERENCE
AUTHORS 3 (bases 1 to 1036)
Genoscope.

TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segre@genoscope.cns.fr - Web :
JOURNAL This GSS is part of a random genomic sequencing program of thirteen
COMMENT yeast species: *Saccharomyces bayanus* var. *uvatum*, *Saccharomyces*
exiguus, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*,

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

Location/Qualifiers

1..1036
/organism="Candida tropicalis"
/mol_type="genomic DNA"
/strain="CBS 94"
/db_xref="taxon:5482"
/clone="BD0A012F03"
/clone_11b="BD0A"
/note="end : T7"
<1..>1036
/note="part of rDNA repeats
contains 35S rDNA"
/evidence=not-experimental

BASE COUNT 272 a 194 c 276 g 291 t 3 others
ORIGIN

Query Match 100.0%; Score 29; DB 29; Length 1036;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCTCAATAAAGACACACACCGATCCC 29
Db 269 GCCTCAATAAAGACACACACCGATCCC 241

RESULT 14
CNS07C91 1038 bp DNA linear GSS 08-JUL-2001
LOCUS T7 end of clone BD0A001A11 of library BD0A from strain CBS 94 of
DEFINITION Candida tropicalis, genomic survey sequence.
ACCESSION AL438892
VERSION AL438892.1 GI:12222305
KEYWORDS GSS.
SOURCE Candida tropicalis
ORGANISM Candida tropicalis

REFERENCE Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
AUTHORS Bolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvéglise,C., Ozler-Kalogeropoulos,O., Potter,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies

TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
PUBMED 11152876

REFERENCE 2 (bases 1 to 1038)
AUTHORS Blandin,G., Ozler-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
Dujon,B.

TITLE Genomic exploration of the hemiascomycetous yeasts: 16. Candida
JOURNAL FEBS Lett. 487 (1), 91-94 (2000)
MEDLINE 20584726
PUBMED 11152891

REFERENCE 3 (bases 1 to 1038)
AUTHORS Genoscope.

TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segref@genoscope.cns.fr - Web :
http://www.genoscope.cns.fr)

COMMENT This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxi.

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

Location/Qualifiers

1..1038
/organism="Candida tropicalis"
/mol_type="genomic DNA"
/strain="CBS 94"
/db_xref="taxon:5482"
/clone="BD0A001A11"
/clone_11b="BD0A"
/note="end : T7"
<1..>1038
/note="part of rDNA repeats
contains 18S rDNA"
/evidence=not-experimental

BASE COUNT 281 a 265 c 197 g 291 t 4 others
ORIGIN

Query Match 100.0%; Score 29; DB 29; Length 1038;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCTCAATAAAGACACACACCGATCCC 29
Db 200 GCCTCAATAAAGACACACACCGATCCC 228

RESULT 15
CNS07CNA 1041 bp DNA linear GSS 08-JUL-2001
LOCUS T3 end of clone BD0A004C06 of library BD0A from strain CBS 94 of
DEFINITION Candida tropicalis, genomic survey sequence.
ACCESSION AL439388
VERSION AL439388.1 GI:12222801
KEYWORDS GSS.
SOURCE Candida tropicalis
ORGANISM Candida tropicalis

REFERENCE Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
AUTHORS Bolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvéglise,C., Ozler-Kalogeropoulos,O., Potter,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies

TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
PUBMED 11152876

REFERENCE 2 (bases 1 to 1041)
AUTHORS Blandin,G., Ozler-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
Dujon,B.

TITLE Genomic exploration of the hemiascomycetous yeasts: 16. Candida
JOURNAL FEBS Lett. 487 (1), 91-94 (2000)
MEDLINE 20584726
PUBMED 11152891

REFERENCE 3 (bases 1 to 1041)
AUTHORS Genoscope.

TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segref@genoscope.cns.fr - Web :
http://www.genoscope.cns.fr)

COMMENT This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxi.

Saccharomyces kluyveri, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

source

1..1041
 location/Qualifiers
 /organism="Candida tropicalis"
 /mol_type="genomic DNA"
 /strain="CBS 94"
 /db_xref="taxon:5482"
 /clone="BD0A004C06"
 /clone_1lb="BD0A"
 /note="end : T3"
 <1..>1041
 /note="part of rDNA repeats
 contains 35S rDNA"
 /evidence="not_experimental"

misc_feature

BASE COUNT 287 a 272 c 198 g 282 t 2 others
 ORIGIN

Query Match

Best Local Similarity 100.0%; Score 29; DB 29; Length 1041;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 GCGTCATTAAGAACAACGATCCC 29
 |||||

Db

414 GCGTCATTAAGAACAACGATCCC 442

Search completed: August 7, 2003, 00:28:26
 Job time : 1570.72 secs


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RESULT 2
US-09-938-842A-5257
; Sequence 5257, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938, 842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 5257
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-5257

Query Match
Best Local Similarity 81.5%; Score 19; DB 10; Length 945;
Pred. No. 2.6e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCGTCATTAAGACAAACACCGATC 27
DB 155 GCATCAACAATAGACAAACACTGTAAC 181

RESULT 3
US-10-239-676-82/c
; Sequence 82, Application US/10239676
; Publication No. US20030082609A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
; FILE REFERENCE: 5013.1003
; CURRENT APPLICATION NUMBER: US/10/239, 676
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/EP01/03968
; DE 10019058.8
; DE 10019173.8
; DE 10032529.7
; DE 10043826.1
; PRIOR FILING DATE: 2001-04-06
; 2000-04-06
; 2000-04-07
; 2000-06-30
; 2000-09-01
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 82
; LENGTH: 9091
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens)
US-10-239-676-82

Query Match
Best Local Similarity 84.0%; Score 18.6; DB 14; Length 9091;
Pred. No. 5.9e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 5 CAATTAAGACAAACACCGATCCC 29
DB 1825 CAATTAAGACAAACACCGATCCC 1801

RESULT 4
US-10-027-632-46818
; Sequence 46818, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027, 632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46818
; LENGTH: 491
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-46818

Query Match
Best Local Similarity 80.8%; Score 18; DB 13; Length 491;
Pred. No. 5.9e+02;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 TCATTAAGACAAACACCGATCCC 29
DB 129 TCATTAAGACAAACACCGATCCC 154

RESULT 5
US-10-027-632-46819
; Sequence 46819, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027, 632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46819
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; LENGTH: 491
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-46819

Query Match
Best Local Similarity 62.1%; Score 18; DB 13; Length 491;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 TCATATAAGACACACACGATCCC 29
DB 129 TCATTCACAAAGACACACAGGATCCC 154

RESULT 6
US-10-027-632-77880
; Sequence 77880, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 77880
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-77880

Query Match
Best Local Similarity 62.1%; Score 18; DB 13; Length 508;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 TCATATAAGACACACACGATCCC 29
DB 129 TCATTCACAAAGACACACAGGATCCC 154

RESULT 7
US-10-027-632-77881
; Sequence 77881, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24

PRIORITY APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 77881
LENGTH: 508
TYPE: DNA
ORGANISM: Human
US-10-027-632-77881

Query Match
Best Local Similarity 62.1%; Score 18; DB 13; Length 508;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 TCATATAAGACACACACGATCCC 29
DB 129 TCATTCACAAAGACACACAGGATCCC 154

RESULT 8
US-10-027-632-314241
; Sequence 314241, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 314241
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-314241

Query Match
Best Local Similarity 62.1%; Score 18; DB 13; Length 508;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 TCATATAAGACACACACGATCCC 29
DB 129 TCATTCACAAAGACACACAGGATCCC 154

RESULT 9
US-10-027-632-314242
; Sequence 314242, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
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; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 314242
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-314242
```

```
Query Match
Best Local Similarity 62.1%; Score 18; DB 13; Length 508;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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```
Qy 4 TCATAAAGACACACACCGATCCC 29
Db 129 TCATTCAGACACACACCGATCCC 154
```

```

RESULT 10
; Sequence 25, Application US/10265689
; Publication No. US20030119775A1
; GENERAL INFORMATION:
; APPLICANT: SURMIT, RICHARD S.
; APPLICANT: COLLINS, SHEILA A.
; APPLICANT: WARDEN, CRAIG H.
; APPLICANT: SELDIN, MICHAEL F.
; APPLICANT: RICQUIER, DANIEL
; APPLICANT: BOULLAUD, FREDERIC
; TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
; FILE REFERENCE: 1579-376
; CURRENT APPLICATION NUMBER: US/10/265,689
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/353,645
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: PCT/US97/06864
; PRIOR FILING DATE: 1997-04-22
; PRIOR APPLICATION NUMBER: 60/034,960
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 9246
; TYPE: DNA
; ORGANISM: Murine sp.
; FEATURE:
; OTHER INFORMATION: "n" bases may be a, t, c, g, modified or unknown
; US-10-265-689-25
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Query Match
Best Local Similarity 62.1%; Score 18; DB 14; Length 9246;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Qy 1 GCGTCATAAAGACACACCGAT 26
Db 2501 GAGGCAATAAATAAACAACACCCCAT 2476
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RESULT 11

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; US-09-764-891-8197
; Sequence 8197, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN ET AL.
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION DATA REMOVED - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8197
; LENGTH: 32167
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-891-8197
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Query Match
Best Local Similarity 62.1%; Score 18; DB 11; Length 32167;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Qy 4 TCATAAAGACACACACCGATCCC 29
Db 20304 TCAGTAAGAGAAAACACACATCCC 20329
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RESULT 12
; US-10-027-632-89343/C
; Sequence 89343, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89343
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-89343
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Query Match
Best Local Similarity 61.4%; Score 17.8; DB 13; Length 567;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
Qy 6 AATAAAGACACACACCGAT 26
Db 389 AATAAAGACACACACTGCT 369
```

```

RESULT 13
; US-10-027-632-303956/C
; Sequence 303956, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
```

```
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; FILE OF INVENTION: Polymorphisms in the Human Genome
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; CURRENT FILING DATE: 2002-04-30
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 303956
;; LENGTH: 567
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-303956
```

```
Query Match          61.4%; Score 17.8; DB 13; Length 567;
Best Local Similarity 90.5%; Pred. No. 7.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

OY 6 AATTAAGACACACACGAT 26
|||||
Db 389 AATTAAGACACACACTGCT 369

```
RESULT 14
US-09-560-863-832/C
;; Sequence 832, Application US/09560863
;; Patent No. US20020110809A1
;; GENERAL INFORMATION:
;; APPLICANT: Nehls, Michael C.
;; APPLICANT: Zambrowicz, Brian
;; APPLICANT: Sands, Arthur T.
;; TITLE OF INVENTION: No. US20020110809A1 Human Polynucleotides and the
;; FILE REFERENCE: LEX-0018-USA
;; CURRENT APPLICATION NUMBER: US/09/560,863
;; CURRENT FILING DATE: 2000-04-28
;; PRIOR APPLICATION NUMBER: US 60/132,408
;; PRIOR FILING DATE: 1999-04-30
;; NUMBER OF SEQ ID NOS: 1008
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 832
;; LENGTH: 634
;; TYPE: DNA
;; ORGANISM: homo sapiens
;; FEATURE:
;; NAME/KEY: misc-feature
;; LOCATION: (1)..(634)
;; OTHER INFORMATION: n = A,T,C or G
US-09-560-863-832
```

```
Query Match          61.4%; Score 17.8; DB 10; Length 634;
Best Local Similarity 86.4%; Pred. No. 7.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

OY 8 TAAAGACACACGATCC 29
|||||
Db 558 TAAAGAAAAAACGATCNC 537

RESULT 15

```
US-10-027-632-216183
;; Sequence 216183, Application US/10027632
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; FILE OF INVENTION: Polymorphisms in the Human Genome
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; CURRENT FILING DATE: 2002-04-30
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 216183
;; LENGTH: 655
;; TYPE: DNA
;; ORGANISM: Human
;; FEATURE:
;; NAME/KEY: misc-feature
;; LOCATION: (1)..(655)
;; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-216183
```

```
Query Match          61.4%; Score 17.8; DB 13; Length 655;
Best Local Similarity 90.5%; Pred. No. 7.5e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

OY 6 AATTAAGACACACACGAT 26
|||||
Db 352 AATTAAGACACACACGAT 372

Search completed: August 7, 2003, 00:32:48
Job time : 115.375 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 6, 2003, 21:25:31 ; Search time 181.25 Seconds

(without alignments)
431.910 Million cell updates/sec

Title: US-09-846-797-1

Perfect score: 29
Sequence: 1 gcgcataaagacacacacgcaccc 29

Scoring table: IDENTITY_NUC
Gap 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: N_Geneseq_19Jun03:*
2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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9: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
10: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
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12: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
13: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
14: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
15: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
16: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
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21: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
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23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
25: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	29	21	AAC81651
2	29	100.0	29	24	AAI70909
3	29	100.0	113	24	AAI70915
4	29	100.0	113	24	AAI70916
5	29	100.0	429	22	AAH21239
6	29	100.0	431	22	AAH21230
7	29	100.0	432	22	AAH21228
8	28	96.6	28	24	AAI70913

C 9	21	72.4	1776	22	AAF25849
C 10	21	72.4	1802	22	AAF23018
C 11	21	72.4	3420	24	ABA99033
C 12	20.2	69.7	568	23	ABV50391
C 13	20	69.0	1078	24	ABQ49302
C 14	20	69.0	1078	24	ABQ49303
C 15	20	69.0	1080	24	ABQ22352
C 16	20	69.0	1080	24	ABQ22353
C 17	19.8	68.3	444	22	AAH21227
C 18	19.8	68.3	2307	22	AAH21227
C 19	19.8	68.3	2307	24	AB231771
C 20	19.8	68.3	4841	16	AAI05696
C 21	19.8	68.3	910715	20	AAH20248
C 22	19.6	67.6	747	24	ABQ41242
C 23	19.6	67.6	747	24	ABQ41243
C 24	19.6	67.6	2707	22	ABL29712
C 25	19.6	67.6	7497	22	AAH46638
C 26	19.6	67.6	7497	24	ABN80251
C 27	19.6	67.6	16545	24	ABL20350
C 28	19.4	66.9	2663	23	ABL24658
C 29	19.4	66.9	2968	23	ABL11176
C 30	19.2	66.2	526	24	ABQ19854
C 31	19.2	66.2	526	24	ABQ19855
C 32	19.2	66.2	8605	24	ABL32534
C 33	19	65.3	945	24	ABL21752
C 34	19	65.5	1798	22	AAD14004
C 35	19	65.5	1798	22	AAD14297
C 36	19	65.5	5319	23	ABL05960
C 37	18.8	64.8	3523	25	ABL10024
C 38	18.8	64.8	6523	24	ABN80121
C 39	18.8	64.8	10020	24	ABL4293
C 40	18.6	64.1	1133	24	ABQ49444
C 41	18.6	64.1	1133	24	ABQ49445
C 42	18.6	64.1	2204	18	AAH84019
C 43	18.6	64.1	5300	24	ABK39946
C 44	18.6	64.1	5300	24	ABL22548
C 45	18.6	64.1	6160	24	ABL70233

ALIGNMENTS

RESULT 1	
AAC81651	
ID AAC81651 standard; DNA; 29 BP.	
AC AAC81651;	
XX	
DT 09-MAR-2001 (first entry)	
XX	
DE Candida sp. rRNA/rDNA hybridisation probe, SEQ ID NO:55.	
XX	
XX	
KW Ribosomal nucleic acid; rRNA; rDNA; microorganism identification;	
KW bacterium; fungus; infection; clinical sample; diagnosis;	
KW nucleic acid matrix; nucleotide array; hybridisation probe; ss.	
XX	
OS Candida albicans.	
OS Candida dubliniensis.	
OS Candida viswanathii.	
OS Candida parapsilosis.	
XX	
PN WO200066789-A2.	
XX	
PD 09-NOV-2000.	
XX	
PF 03-MAY-2000; 2000MO-US12421.	
XX	
PR 03-MAY-1999; 99US-0132411.	
XX	
PR 20-AUG-1999; 99US-0150149.	
XX	
PA (GENP-) GEN-PROBE INC.	
XX	

S. exiguus 18S rRNA
Yeast 18S rRNA seq
Saccharomyces cere
Human prostate exp
Oligonucleotide fo
Oligonucleotide fo
Oligonucleotide fo
Oligonucleotide fo
T. glabrata 16S rR
Candida albicans e
Candida albicans e
Plax rust resistan
Borrelia burgdorfe
Oligonucleotide fo
Oligonucleotide fo
Tumour suppressor
Human chemically m
Human immune syste
Drosophila melanog
Drosophila melanog
Oligonucleotide fo
Oligonucleotide fo
Human immune syste
Arabidopsis thaliana
DNA to infer yeast
Yeast DNA to infer
Drosophila melanog
Hemtopoietic cel
Human chemically m
Human immune syste
Oligonucleotide fo
Oligonucleotide fo
DNA encoding a Sta
Human chemically p
Human immune syste
Chemically treated

```

PI Hogan JT;
XX
XX WPI; 2000-687550/67.
XX
XX A device for hybridizing nucleic acids useful for identifying
PT microorganisms comprises a solid support and several addresses
PT comprising a probe, disposed on the solid support
XX
XX Disclosure; Page 40; 96pp; English.
XX
XX The invention relates to a nucleotide matrix for the identification
CC of microorganisms, and a method of identifying the microorganisms(s)
CC in a biological sample using the nucleotide matrix. The matrix comprises
CC a collection of nucleic acid hybridisation probes, with each probe being
CC specific for the ribosomal nucleic acids (rRNA or rDNA) of at least one
CC microorganism (e.g., a bacterium or a fungus). The collection of probes
CC is organised into a series of "addresses" that provide information about
CC the presence or absence of one or more nucleotide sequences in the
CC biological sample. Probes in the matrix are selected to distinguish
CC between organisms that differ from each other by a known phylogenetic
CC relationship. The addresses include a higher order address (the least
CC organism-specific address which is able to bind to a ribosomal nucleic
CC acid from a broad class of organisms e.g., one common to all fungi), an
CC intermediate address and a lower order address (the most organism-
CC specific). The lower order address hybridises rRNA/rDNA from a subset of
CC organisms whose ribosomal nucleic acids hybridise to the intermediate
CC order address. Likewise, the intermediate order address hybridises
CC ribosomal nucleic acids from a subset of organisms having ribosomal
CC nucleic acids that hybridise at the higher order address. The method and
CC nucleic acid matrix of the invention is used for identifying
CC microorganisms, especially in clinical samples. The method can detect
CC and resolve the identities of microorganisms that are present in a mixed
CC sample. The system is suited to automated analysis, and enables the
CC identification of a disease-causing microorganism without the need for
CC experienced technicians. The present sequence represents a ribosomal
CC nucleic acid-specific hybridisation probe for use in a nucleic acid
CC matrix of the invention.
XX
XX Sequence 29 BP; 13 A; 9 C; 4 G; 3 T; 0 other;
SQ
Query Match 100.0%; Score 29; DB 21; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GCGTCATTAAGAAGACACACACCGATCCC 29
DB 1 GCGTCATTAAGAAGACACACACCGATCCC 29
RESULT 2
AA170909
ID AA170909 standard; DNA; 29 BP.
XX
XX AA170909;
AC
XX 12-MAR-2002 (first entry)
DT
XX
XX Probe CALA1037 for Candida species detection and quantitation.
DE
XX
XX Candida albicans; Candida tropicalis; Candida dubliniensis;
KW Candida viswanathii; Candida parapsilosis; detection; probe; ss.
XX
XX Candida albicans.
OS
XX WO200183821-A2.
XX
XX 08-NOV-2001.
PD
XX
XX 01-MAY-2001; 2001WO-US13884.
PF
XX 01-MAY-2000; 2000US-201249P.
PR
XX (GENP-) GEN-PROBE INC.
PA

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XX
XX Hogan JT, Gordon PC;
XX
XX WPI; 2002-066537/09.
XX
XX Novel oligonucleotide sequences that are fully complementary to
PT ribosomal RNA or DNA of Candida species, useful for detecting presence
PT of C.albicans, C.dubliniensis, C.viswanathii, C.parapsilosis in test
PT sample
XX
XX Claim 2; Page 19; 33pp; English.
XX
XX The present sequence is that of oligonucleotide probe CALA1037,
CC which is complementary to a unique segment (see AA170916) of the
CC 18S ribosomal RNA of Candida albicans, Candida tropicalis, Candida
CC dubliniensis, Candida viswanathii and Candida tropicalis. The
CC probe is highly specific, and can distinguish these Candida species
CC from their known phylogenetically nearest neighbours. It is
CC useful for their detection and quantitation. Probe CALA1037 is
CC 29 bases in length, has a Tm of 59.5 degree C, and hybridises rRNA
CC in a manner that is enhanced by the presence of helper
CC oligonucleotides (see AA170910-12). The probe is an illustration of
CC an oligonucleotide that: (1) hybridises the target nucleic acid under
CC high stringency hybridisation conditions; (2) has a length of up to
CC 100 nucleotide bases; and (3) includes at least 15 contiguous
CC nucleotides falling within the sequence given in AA170915 or its
CC complement. It may include a detectable moiety, such as an
CC acridinium ester or a radioisotope.
XX
XX Sequence 29 BP; 13 A; 9 C; 4 G; 3 T; 0 other;
SQ
Query Match 100.0%; Score 29; DB 24; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GCGTCATTAAGAAGACACACACCGATCCC 29
DB 1 GCGTCATTAAGAAGACACACACCGATCCC 29
RESULT 3
AA170915
ID AA170915 standard; DNA; 113 BP.
XX
XX AA170915;
AC
XX 12-MAR-2002 (first entry)
DT
XX
XX Candida species 18S ribosomal DNA probe domain.
DE
XX
XX Candida albicans; Candida tropicalis; Candida dubliniensis;
KW Candida viswanathii; Candida parapsilosis; detection; probe; ss.
XX
XX Candida albicans.
OS
XX WO200183821-A2.
XX
XX 08-NOV-2001.
PD
XX
XX 01-MAY-2001; 2001WO-US13884.
PF
XX 01-MAY-2000; 2000US-201249P.
PR
XX (GENP-) GEN-PROBE INC.
PA Hogan JT, Gordon PC;
XX
XX WPI; 2002-066537/09.
XX
XX Novel oligonucleotide sequences that are fully complementary to
PT ribosomal RNA or DNA of Candida species, useful for detecting presence
PT of C.albicans, C.dubliniensis, C.viswanathii, C.parapsilosis in test
PT sample

```

XX Claim 1; Page 32; 33pp; English.

PS The present sequence is that of DNA corresponding to a unique
CC segment (see AA170916) of the 18S ribosomal RNA of *Candida albicans*,
CC *Candida tropicalis*, *Candida dubliniensis*, *Candida viswanathii* and
CC *Candida tropicalis*. Claimed hybridisation probes and helper
CC oligonucleotides (see AA170909-14) correspond to a portion of this
CC sequence or its complement. The probes are highly specific, and can
CC distinguish *Candida* species from their known phylogenetically
CC nearest neighbours. They are useful for detection and quantitation.
XX

Sequence 113 BP; 35 A; 27 C; 23 G; 28 T; 0 other;

Query Match 100.0%; Score 29; DB 24; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCGTCATTAAGAACACACCGATCCC 29
DB 42 GCGTCATTAAGAACACACCGATCCC 70

RESULT 4

AA170916/c
ID AA170916 standard; rRNA; 113 BP.

AA170916;

12-MAR-2002 (first entry)

Candida species 18S ribosomal RNA probe domain.

Candida albicans; *Candida tropicalis*; *Candida dubliniensis*;

Candida viswanathii; *Candida parapsilosis*; detection; probe; ss.

Candida albicans.

WO200183821-A2.

08-NOV-2001.

01-MAY-2001; 2001MO-US13884.

01-MAY-2000; 2000US-201249P.

(GENP-) GEN-PROBE INC.

Hogan JJ, Gordon PC;

WPI; 2002-066537/09.

Novel oligonucleotide sequences that are fully complementary to
PT ribosomal RNA or DNA of *Candida* species, useful for detecting presence
PT of *C. albicans*, *C. dubliniensis*, *C. viswanathii*, *C. parapsilosis* in test
PT sample.
XX Disclosure; Page 32; 33pp; English.

XX The present sequence is that of a unique segment of the 18S
CC ribosomal RNA of *Candida albicans*, *Candida tropicalis*,
CC *Candida dubliniensis*, *Candida viswanathii* and *Candida tropicalis*.
CC Claimed hybridisation probes and helper oligonucleotides (see
CC AA170909-14) correspond to a portion of this sequence or its
CC complement. The probes are highly specific, and can distinguish
CC these *Candida* species from their known phylogenetically nearest
CC neighbours. They are useful for detection and quantitation.
XX

Sequence 113 BP; 28 A; 23 C; 27 G; 35 U; 0 other;

Query Match 100.0%; Score 29; DB 24; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCGTCATTAAGAACACACCGATCCC 29
DB 72 GCGTCATTAAGAACACACCGATCCC 44

RESULT 5

AAH21229/c
ID AAH21229 standard; DNA; 429 BP.

AAH21229;

13-SEP-2001 (first entry)

C. tropicalis 16S rRNA DNA fragment YSASRUG.

Hybridization; diagnosis; bacterial infection; sepsis; fungal infection;
KM food monitoring; water monitoring; veterinary; forensic; primer; probe;
KM detection; ss.

Candida tropicalis.

WO200148237-A2.

05-JUL-2001.

27-DEC-2000; 2000MO-DE04610.

23-DEC-1999; 99DE-1062895.

31-MAY-2000; 2000DE-1027113.

(HOEF/) HOEF A.

(STUE/) STUEBER F.

Hoef A, Stueber F;

WPI; 2001-425677/45.

Rapid determination of microbial nucleic acid, useful e.g. for
PT diagnosing bacterial infections, by analysis of temperature-dependent
PT hybridization with oligonucleotides
XX
XX Disclosure; Figure 13; 57pp; German.

XX This invention describes a novel method for detecting microbial DNA/RNA
CC (1) by concentrating (1) from a sample, adding at least one labeled
CC oligonucleotide (ON), performing temperature-dependent hybridization and
CC determining (1) from the physical properties of the (1)-ON complex, e.g.
CC the temperature dependence of hybridization. The method is used for rapid
CC determination of microbial genomic RNA or DNA, particularly for diagnosis
CC of bacterial infections (e.g. sepsis) or fungal infections (particularly
CC in intensive care patients), also for monitoring food and water, and for
CC veterinary or forensic investigations. The method provides quick
CC (typically less than 3 hours) quantitative and qualitative
CC determination/identification of microbial nucleic acid. It is very
CC sensitive, allowing early diagnosis of infection. AAH21160-AAH21231
CC represent primers and probes used to illustrate the method of the
CC invention.
XX

Sequence 429 BP; 114 A; 85 C; 109 G; 119 T; 2 other;

Query Match 100.0%; Score 29; DB 22; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCGTCATTAAGAACACACCGATCCC 29
DB 408 GCGTCATTAAGAACACACCGATCCC 380

RESULT 6

AAH21230/c
ID AAH21230 standard; DNA; 431 BP.


```

XX AAH21230;
AC 13-SEP-2001 (first entry)
XX
XX DE C. albicans 16S rRNA DNA fragment YSASRSUA.
XX Hybridization; diagnosis; bacterial infection; sepsis; fungal infection;
XX food monitoring; water monitoring; veterinary; forensic; primer; probe;
XX detection; ss.
XX
XX OS Candida albicans.
XX
XX PN WO200148237-A2.
XX
XX PD 05-JUL-2001.
XX
XX PE 27-DEC-2000; 2000WO-DE04610.
XX
XX PR 23-DEC-1999; 99DE-1062895.
XX PR 31-MAY-2000; 2000DE-1027113.
XX
XX PA (HOEF/) HOEFT A.
XX PA (STUE/) STUEBER F.
XX
XX PI Hoeft A, Stueber F;
XX
XX DR WPI; 2001-425677/45.
XX
XX PT Rapid determination of microbial nucleic acid, useful e.g. for
XX PT diagnosing bacterial infections, by analysis of temperature-dependent
XX PT hybridization with oligonucleotides
XX
XX PS Disclosure; Figure 13; 57pp; German.
XX
XX CC This invention describes a novel method for detecting microbial DNA/RNA
XX CC (I) by concentrating (I) from a sample, adding at least one labeled
XX CC oligonucleotide (ON), performing temperature-dependent hybridization and
XX CC determining (I) from the physical properties of the (I)-ON complex, e.g.
XX CC the temperature dependence of hybridization. The method is used for rapid
XX CC determination of microbial genomic RNA or DNA, particularly for diagnosis
XX CC of bacterial infections (e.g. sepsis) or fungal infections (particularly
XX CC in intensive care patients), also for monitoring food and water, and for
XX CC veterinary or forensic investigations. The method provides quick
XX CC (typically less than 3 hours) quantitative and qualitative
XX CC determination/identification of microbial nucleic acid. It is very
XX CC sensitive, allowing early diagnosis of infection. AAH21160-AAH21231
XX CC represent primers and probes used to illustrate the method of the
XX CC invention.
XX
XX SQ Sequence 431 BP; 115 A; 86 C; 110 G; 120 T; 0 other;

Query Match 100.0%; Score 29; DB 22; Length 431;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTCAATTAAGACACACACCGATCCC 29
   |||||||||||||||||||||||||||
DB 410 GCCTCAATTAAGACACACACCGATCCC 382

RESULT 7
AAH21228/c
ID AAH21228 standard; DNA; 432 BP.
XX
XX AC AAH21228;
XX
XX DT 13-SEP-2001 (first entry)
XX
XX DE C. parapsilosis 16S rRNA DNA fragment YSASRSUF.
XX
XX KM Hybridization; diagnosis; bacterial infection; sepsis; fungal infection;
XX KM food monitoring; water monitoring; veterinary; forensic; primer; probe;

```

```

KM detection; ss.
XX
XX OS Candida parapsilosis.
XX
XX PN WO200148237-A2.
XX
XX PD 05-JUL-2001.
XX
XX PE 27-DEC-2000; 2000WO-DE04610.
XX
XX PR 23-DEC-1999; 99DE-1062895.
XX PR 31-MAY-2000; 2000DE-1027113.
XX
XX PA (HOEF/) HOEFT A.
XX PA (STUE/) STUEBER F.
XX
XX PI Hoeft A, Stueber F;
XX
XX DR WPI; 2001-425677/45.
XX
XX PT Rapid determination of microbial nucleic acid, useful e.g. for
XX PT diagnosing bacterial infections, by analysis of temperature-dependent
XX PT hybridization with oligonucleotides
XX
XX PS Disclosure; Figure 13; 57pp; German.
XX
XX CC This invention describes a novel method for detecting microbial DNA/RNA
XX CC (I) by concentrating (I) from a sample, adding at least one labeled
XX CC oligonucleotide (ON), performing temperature-dependent hybridization and
XX CC determining (I) from the physical properties of the (I)-ON complex, e.g.
XX CC the temperature dependence of hybridization. The method is used for rapid
XX CC determination of microbial genomic RNA or DNA, particularly for diagnosis
XX CC of bacterial infections (e.g. sepsis) or fungal infections (particularly
XX CC in intensive care patients), also for monitoring food and water, and for
XX CC veterinary or forensic investigations. The method provides quick
XX CC (typically less than 3 hours) quantitative and qualitative
XX CC determination/identification of microbial nucleic acid. It is very
XX CC sensitive, allowing early diagnosis of infection. AAH21160-AAH21231
XX CC represent primers and probes used to illustrate the method of the
XX CC invention.
XX
XX SQ Sequence 432 BP; 114 A; 86 C; 110 G; 121 T; 1 other;

Query Match 100.0%; Score 29; DB 22; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTCAATTAAGACACACACCGATCCC 29
   |||||||||||||||||||||||||||
DB 411 GCCTCAATTAAGACACACACCGATCCC 383

RESULT 8
AAI70913
ID AAI70913 standard; DNA; 28 BP.
XX
XX AC AAI70913;
XX
XX DT 12-MAR-2002 (first entry)
XX
XX DE Probe CALA1038 for Candida species detection and quantitation.
XX
XX KM Candida albicans; Candida tropicalis; Candida dubliniensis;
XX KM Candida viswanathii; Candida parapsilosis; detection; probe; ss.
XX
XX OS Candida albicans.
XX
XX PN WO200183821-A2.
XX
XX PD 08-NOV-2001.
XX
XX PF 01-MAY-2001; 2001WO-US13884.
XX

```


PT Preparing a probe for nucleic acid hybridization assays comprises
 PT constructing a nucleotide polymer sufficiently complementary to
 PT hybridize to an RNA region that distinguishes non-viral target from
 PT non-viral non-target species -
 XX
 XX
 PS Disclosure: Fig 4; 75pp; English.
 XX
 CC The present invention provides novel methods of producing probes for use
 CC in the identification of a number of microorganisms. These include E.
 CC coli, Mycobacteria, Mycoplasma, Campylobacter, Chlamydia, Enterobacter,
 CC Legionella, Salmonella, Pseudomonas, Neisseria gonorrhoeae, fungi and
 CC bacteria.
 XX
 SQ Sequence 1802 BP; 479 A; 351 C; 462 G; 510 U; 0 other;
 Query Match 72.4%; Score 21; DB 22; Length 1802;
 Best Local Similarity 82.8%; Pred. No. 53;
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 OY 1 GCGTCATTAAGAAACACACCGATCCC 29
 Db 1067 GGGTCATTAAAAAACACACCGATCCC 1039
 RESULT 11
 ID ABA99033 standard; DNA; 3420 BP.
 XX
 AC ABA99033;
 XX
 DT 20-MAY-2002 (first entry)
 XX
 DE Saccharomyces cerevisiae chromosome XII cosmid reading frame ORF YLR154c.
 XX
 KW Eco2.0; tree lineage; fibre length; wood density; fibre collapsibility;
 KW fibre coarseness; growth rate; cell wall thickness; lignin content;
 KW guaiacyl lignin content; syringyl lignin content; carbohydrate content;
 KW kraft pulp yield; mechanical pulp energy demand; chemical pulping; fibre
 KW quality; wood quality; YLR154c; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 878..10537
 FT /*tag= a
 FT /note= "Eco2.0 probe complete sequence"
 XX
 PN WO200204663-A2.
 XX
 PD 17-JAN-2002.
 XX
 PF 21-JUN-2001; 2001WO-CA00927.
 XX
 PR 23-JUN-2000; 2000US-213585P.
 XX
 PA (PPCA) PULP & PAPER RES INST CANADA.
 XX
 PI Potter S, Watson PA;
 XX
 DR WPI: 2002-179711/23.
 XX
 XX Identifying tree lineage for identifying trees having superior
 PT phenotype, e.g. fibre length, comprises hybridizing a DNA probe to tree
 PT genomic DNA isolated from spruce live tissue and assessing intensity of
 PT the hybridization pattern -
 XX
 PS Disclosure: Fig 4; 48pp; English.
 XX
 CC The sequence represents a fragment of Saccharomyces cerevisiae chromosome
 CC XII cosmid reading frame ORF YLR154c, including the complete sequence of
 CC the Eco2.0 probe. The invention relates to a novel method for identifying
 CC tree lineage capable of expressing desired biological and/or biochemical
 CC phenotypes. The method is useful for identifying trees having superior

CC phenotype, including fibre length, wood density, fibre collapsibility,
 CC fibre coarseness, cell wall thickness, growth rate, lignin content,
 CC guaiacyl lignin content, syringyl lignin content, carbohydrate content,
 CC kraft pulp yield, mechanical pulp energy demand, chemical uptake for
 CC chemical pulping, extractive content and extractive compounds. The trees
 CC include trees of the genus Pichia, Populus, Betula, Abies, Larix, Taxus,
 CC Ulmus, Prunus, Quercus, Malus, Arbutus, Salix, Platanus, Acer, Tsuga,
 CC Pseudotsuga, Pinus, Firaxinus, Eucalyptus, Acacia, Abrus, Cupressus,
 CC Fagus, Juniperus, Thuja and Carya. The Eco2.0 probe is useful for
 CC predicting wood or fibre quality.
 XX
 SQ Sequence 3420 BP; 1007 A; 853 C; 621 G; 939 T; 0 other;
 Query Match 72.4%; Score 21; DB 24; Length 3420;
 Best Local Similarity 82.8%; Pred. No. 55;
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 OY 1 GCGTCATTAAGAAACACACCGATCCC 29
 Db 1590 GGGTCATTAAAAAACACACCGATCCC 1618
 RESULT 12
 ID ABV50391 standard; cDNA; 568 BP.
 XX
 AC ABV50391;
 XX
 DT 17-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 50382.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-218007P.
 PR 13-DEC-2000; 2000US-235281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI: 2001-662795/76.
 XX
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 PS Claim 1; Page 9808; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;

CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 568 BP; 211 A; 109 C; 85 G; 162 T; 1 other;
Query Match 69.7%; Score 20.2; DB 23; Length 568;
Best Local Similarity 88.0%; Pred. No. 1e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GCGTCATTAAGAACACACCGA 25
DB 55 GCGTATTTAAAGAACACACCGA 79
RESULT 13
ABQ49302/C
ID ABQ49302 standard; DNA: 1078 BP.
XX
AC ABQ49302;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 35893.
XX
KW Human; cytosine methylation; 5'-CPG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PE 01-SEP-2001; 2001WO-EP10074.
XX
PF 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI: 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CPG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC member of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP/s); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in

CC the disclosure of the invention.
XX
SQ Sequence 1078 BP; 154 A; 128 C; 385 G; 411 T; 0 other;
Query Match 69.0%; Score 20; DB 24; Length 1078;
Best Local Similarity 82.1%; Pred. No. 1.3e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 CGTCATTAAGAACACACCGATCCC 29
DB 902 CGATTAATAAAGAACACACCGATCCC 875
RESULT 14
ABQ49303
ID ABQ49303 standard; DNA: 1078 BP.
XX
AC ABQ49303;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 35894.
XX
KW Human; cytosine methylation; 5'-CPG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PE 01-SEP-2001; 2001WO-EP10074.
XX
PF 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI: 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CPG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC member of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP/s); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
SQ Sequence 1078 BP; 411 A; 385 C; 128 G; 154 T; 0 other;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 6, 2003, 21:26:11 ; Search time 710.047 Seconds

(without alignments)
1670.846 Million cell updates/sec

Title: US-09-846-797-1

Perfect score: 29

Sequence: 1 ggcgcataaagacacacacacgaccc 29

Scoring table:

IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	29	AX045494	AX045494 Sequence
2	29	100.0	29	AX298059	AX298059 Sequence
3	29	100.0	113	AX298065	AX298065 Sequence
4	29	100.0	113	AX298066	AX298066 Sequence
5	29	100.0	510	AF247474	AF247474 Unidentif
6	29	100.0	1029	AB030915	AB030915 Candida p
7	29	100.0	1632	AF114470	AF114470 Candida a
8	29	100.0	1670	AY227019	AY227019 Candida p
9	29	100.0	1700	CAJ5123	CAJ5123 Candida p
10	29	100.0	1723	VSASRSUH	VSASRSUH Candida a
11	29	100.0	1736	VSASRSUF	VSASRSUF Candida a
12	29	100.0	1739	VSASRSUF	VSASRSUF Candida a
13	29	100.0	1766	AB013533	AB013533 Candida l
14	29	100.0	1767	AB013549	AB013549 Candida s
15	29	100.0	1768	AB013589	AB013589 Candida v
16	29	100.0	1769	AB013586	AB013586 Candida a
17	29	100.0	1769	AB013588	AB013588 Candida a
18	29	100.0	1782	AY055856	AY055856 Candida p
19	29	100.0	1783	AY055855	AY055855 Candida p
20	29	100.0	1783	AY055857	AY055857 Candida p
21	29	100.0	1785	VSASRRNB	VSASRRNB Candida p
22	29	100.0	1787	VSASRSUA	VSASRSUA Candida tro
23	29	100.0	1788	AK069785	AK069785 Sequence
24	29	100.0	1788	EL5168	EL5168 Candida alb
25	29	100.0	1788	CAL165	CAL165 Candida alb
26	29	100.0	1791	CD18SRNA	CD18SRNA Candida alb
27	28	96.6	28	AX298063	AX298063 Sequence
28	27.4	94.5	741	AF290987S2	AF290987S2 Sequence
29	27.4	94.5	1747	AB054292	AB054292 Candida t
30	27.4	94.5	1753	LECB518SR	LECB518SR Candida sp
31	27.4	94.5	1772	AB013529	AB013529 Candida s
32	27.4	94.5	1773	AB013560	AB013560 Candida s
33	25.8	89.0	1020	AB030914	AB030914 Candida a
34	25.8	89.0	1038	AB030913	AB030913 Candida a
35	25.8	89.0	1043	AB030913	AB030913 Candida a
36	25.8	89.0	1043	AB030913	AB030913 Candida a
37	25.8	89.0	1043	AB030913	AB030913 Candida a
38	25.8	89.0	1043	AB030913	AB030913 Candida a
39	25.8	89.0	1043	AB030913	AB030913 Candida a
40	25.8	89.0	1043	AB030913	AB030913 Candida a
41	25.8	89.0	1043	AB030913	AB030913 Candida a
42	25.8	89.0	1043	AB030913	AB030913 Candida a
43	25.8	89.0	1043	AB030913	AB030913 Candida a
44	25.8	89.0	1043	AB030913	AB030913 Candida a
45	25.8	89.0	1043	AB030913	AB030913 Candida a

ALIGNMENTS

RESULT 1
AX045494
LOCUS AX045494 29 bp DNA
DEFINITION Sequence 55 from Patent WO0066789.
ACCESSION AX045494
VERSION AX045494.1 GI:11343957
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Hogan, J.J.
TITLE Polynucleotide matrix-based method of identifying microorganisms
JOURNAL Patent: WO 0066789-A 55 09-NOV-2000;
Gen-Probe Incorporated (US)

Pred. No. 15 is the number of results predicted by chance to have a

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FEATURES
  source
    Location/Qualifiers
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        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
        /note="Probe for hybridizing ribosomal nucleic acids of a
        plurality of fungi in the genus Candida"
BASE COUNT      13 a          9 c          4 g          3 t
ORIGIN

Query Match      100.0%; Score 29; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCTCAATAAAGACACACACCGATCCC 29
    |||
Db 1 GCCTCAATAAAGACACACACCGATCCC 29

RESULT 2
AX298059
LOCUS      AX298059      29 bp      DNA      linear      PAT 26-NOV-2001
DEFINITION Sequence 1 from Patent WO0183821.
ACCESSION AX298059
VERSION   AX298059.1 GI:17128145
KEYWORDS
SOURCE    Candida albicans
ORGANISM  Candida albicans
REFERENCE 1
  AUTHORS  Hogan, J.J. and Gordon, P.C.
  TITLE    Polynucleotide probes for detection and quantitation of Candida
  JOURNAL  Patent: WO 0183821-A 1 08-NOV-2001;
  FEATURES Location/Qualifiers
    source
      1..29
        /organism="Candida albicans"
        /mol_type="genomic DNA"
        /db_xref="taxon:5476"
BASE COUNT      13 a          9 c          4 g          3 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCTCAATAAAGACACACACCGATCCC 29
    |||
Db 1 GCCTCAATAAAGACACACACCGATCCC 29

RESULT 3
AX298065
LOCUS      AX298065      113 bp      DNA      linear      PAT 26-NOV-2001
DEFINITION Sequence 7 from Patent WO0183821.
ACCESSION AX298065
VERSION   AX298065.1 GI:17128151
KEYWORDS
SOURCE    Candida albicans
ORGANISM  Candida albicans
REFERENCE 1
  AUTHORS  Hogan, J.J. and Gordon, P.C.
  TITLE    Polynucleotide probes for detection and quantitation of Candida
  JOURNAL  Patent: WO 0183821-A 7 08-NOV-2001;
  FEATURES Location/Qualifiers
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      1..113
        /organism="Candida albicans"

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    misc_structure 1..113
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BASE COUNT      35 a          27 c          23 g          28 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCTCAATAAAGACACACACCGATCCC 29
    |||
Db 42 GCCTCAATAAAGACACACACCGATCCC 70

RESULT 4
AX298066/c
LOCUS      AX298066      113 bp      mRNA      linear      PAT 26-NOV-2001
DEFINITION Sequence 8 from Patent WO0183821.
ACCESSION AX298066
VERSION   AX298066.1 GI:17128152
KEYWORDS
SOURCE    Candida albicans
ORGANISM  Candida albicans
REFERENCE 1
  AUTHORS  Hogan, J.J. and Gordon, P.C.
  TITLE    Polynucleotide probes for detection and quantitation of Candida
  JOURNAL  Patent: WO 0183821-A 8 08-NOV-2001;
  FEATURES Location/Qualifiers
    source
      1..113
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        /mol_type="mRNA"
        /db_xref="taxon:5476"
BASE COUNT      28 a          23 c          27 g          35 t
ORIGIN

Query Match      100.0%; Score 29; DB 6; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCTCAATAAAGACACACACCGATCCC 29
    |||
Db 72 GCCTCAATAAAGACACACACCGATCCC 44

RESULT 5
AF247474/c
LOCUS      AF247474      510 bp      DNA      linear      PLN 06-FEB-2003
DEFINITION Unidentified saccharomycetalean sp. SPT1 18S ribosomal RNA, partial
sequence.
ACCESSION AF247474
VERSION   AF247474.1 GI:7716602
KEYWORDS
SOURCE    saccharomycete isolate SPT1
ORGANISM  saccharomycete isolate SPT1
REFERENCE 1
  AUTHORS  Trosok, S.P., Luong, J.H., Juck, D.F. and Driscoll, B.T.
  TITLE    Characterization of two novel yeast strains used in mediated
  JOURNAL  biosensors for wastewater
  MEDLINE  Can. J. Microbiol. 48 (5), 418-426 (2002)
  PUBMED  22104291
  MEDLINE  12109881
  PUBMED  2 (bases 1 to 510)
REFERENCE 2
  AUTHORS  Trosok, S.P., Driscoll, B.T. and Luong, J.H.

```

TITLE Direct Submission
JOURNAL Submitted (20-MAR-2000) Natural Resource Sciences, McGill University, 21,111 Lakeshore Rd., Ste-Anne-de-Bellevue, PQ H9X 3V9, Canada

FEATURES
SOURCE Location/Qualifiers
 1. 510
 /organism="Saccharomycete isolate SP1"
 /mol_type="genomic DNA"
 /isolate="SP1"
 /db_xref="taxon:123505"
 /country="Canada: Quebec, Thurso"
 /note="Isolated from pulp mill effluent"
 <1..>510
 /product="18S ribosomal RNA"

BASE COUNT 139 a 87 c 126 g 158 t

ORIGIN

Query Match 100.0%; Score 29; DB 8; Length 510;
 Best Local Similarity 100.0%; Pred. No. 0.27;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGTCATTAAGAACACACCGATCCC 29
 |||||
 462 GCGTCATTAAGAACACACCGATCCC 434

Db 462 GCGTCATTAAGAACACACCGATCCC 434

RESULT 6
LOCUS AB030915 1029 bp DNA linear PLN 19-AUG-1999
DEFINITION Candida parapsilosis gene for 18S rRNA, partial sequence.
ACCESSION AB030915
VERSION 1 GI:5738919
KEYWORDS 18S rRNA; 18S ribosomal RNA.
SOURCE Candida parapsilosis
ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.

REFERENCE 1 (bases 1 to 1029)
AUTHORS Shintani, T. and Matsumoto, Y.
JOURNAL Candida parapsilosis gene for 18S rRNA, partial sequence
REFERENCE 2 (bases 1 to 1029)
AUTHORS Shintani, T. and Matsumoto, Y.
JOURNAL Direct Submission
 Submitted (10-AUG-1999) Tomoyoshi Shintani, Industrial Research Center of Ehime Prefecture, Laboratory of Food Process, 487-2 Kumekebota, Matsuyama, Ehime 791-1101, Japan
 (E-mail:shintani@rl.pref.ehime.jp, URL:www.iri.pref.ehime.jp, Tel:81-89-976-7612, Fax:81-89-976-7313)

FEATURES
SOURCE Location/Qualifiers
 1. 1029
 /organism="Candida parapsilosis"
 /mol_type="genomic DNA"
 /strain="IEY2"
 /db_xref="taxon:5480"
 <1..>1029
 /product="18S ribosomal RNA"

BASE COUNT 291 a 195 c 249 g 294 t

ORIGIN

Query Match 100.0%; Score 29; DB 8; Length 1029;
 Best Local Similarity 100.0%; Pred. No. 0.25;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGTCATTAAGAACACACCGATCCC 29
 |||||
 1010 GCGTCATTAAGAACACACCGATCCC 982

Db 1010 GCGTCATTAAGAACACACCGATCCC 982

RESULT 7
LOCUS AF114470 1632 bp DNA linear PLN 25-MAR-1999
DEFINITION Candida albicans 18S ribosomal RNA gene, complete sequence.

ACCESSION AF114470
VERSION AF114470.1 GI:4512045
KEYWORDS Candida albicans
SOURCE Candida albicans
ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.

REFERENCE 1 (bases 1 to 1632)
AUTHORS Morris, M. L., Andrews, R. H., Rogers, A. H. and Ellis, D. H.
JOURNAL 18S rRNA gene full sequence for the type strain of Candida albicans, CBS 562
 Unpublished

REFERENCE 2 (bases 1 to 1632)
AUTHORS Morris, M. L., Andrews, R. H., Rogers, A. H. and Ellis, D. H.
JOURNAL Direct Submission
 Submitted (16-DEC-1998) Dentistry, University of Adelaide, North Terrace, Adelaide, SA 5005, Australia

FEATURES
SOURCE Location/Qualifiers
 1. 1632
 /organism="Candida albicans"
 /mol_type="genomic DNA"
 /strain="CBS 562"
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BASE COUNT 433 a 319 c 427 g 452 t

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 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGTCATTAAGAACACACCGATCCC 29
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 948 GCGTCATTAAGAACACACCGATCCC 920

Db 948 GCGTCATTAAGAACACACCGATCCC 920

RESULT 8
LOCUS AY227019 1670 bp DNA linear PLN 01-APR-2003
DEFINITION Candida parapsilosis strain CCO 3 18S ribosomal RNA gene, partial sequence.
ACCESSION AY227019
VERSION 1 GI:29423630
KEYWORDS Candida parapsilosis
SOURCE Candida parapsilosis
ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.

REFERENCE 1 (bases 1 to 1670)
AUTHORS Sujaya, I. N., Tamura, Y., Tanaka, T., Yamaki, T., Ikeda, T., Kikushima, N., Yata, H., Yokota, A., Asano, K. and Tomita, F.
JOURNAL Molecular monitoring of Zygosaccharomyces rouxii strain M2 in miso fermentation
 Unpublished

REFERENCE 2 (bases 1 to 1670)
AUTHORS Sujaya, I. N., Tamura, Y., Tanaka, T., Yamaki, T., Ikeda, T., Kikushima, N., Yata, H., Yokota, A., Asano, K. and Tomita, F.
JOURNAL Direct Submission
 Submitted (29-JAN-2003) Molecular Bioscience, Grad. Sch. of Agric. Hokkaido University, North 9 West 9, Sapporo, Hokkaido 0608589, Japan

FEATURES
SOURCE Location/Qualifiers
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 /mol_type="genomic DNA"
 /strain="CCO 3"
 /db_xref="taxon:5480"
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BASE COUNT 449 a 328 c 432 g 461 t

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTCAATAAAGACACACACCGATCCC 29
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 Db 968 GCCTCAATAAAGACACACACCGATCCC 940

RESULT 9
 CAAJ5123 1700 bp DNA linear PLN 02-FEB-1999
 LOCUS Candida albicans SSU rRNA gene.
 DEFINITION AJ005123
 VERSION AJ005123.1 GI:3046725
 KEYWORDS small subunit ribosomal RNA; SSU rRNA gene.
 SOURCE Candida albicans
 ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; mitosporic Saccharomycetales; Candida.

REFERENCE 1
 AUTHORS Kerkmann, M.L., Schuppeler, M., Paul, K.D., Schoenian, G. and Smith, M.T.
 TITLE Red-pigmented Candida albicans in patients with cystic fibrosis
 JOURNAL J. Clin. Microbiol. 37 (1), 278 (1999)
 MEDLINE 99136628
 PUBMED 9988594

REFERENCE 2 (bases 1 to 1700)
 AUTHORS Schuppeler, M.
 TITLE Direct Submission
 SUBMITTED (08-APR-1998) Schuppeler M., Medizinische Mikrobiologie
 und Hygiene, Universitätsklinikum der TU-Dresden, Duererstrasse
 24, D-01307 Dresden, GERMANY
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 <1. >1700
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 /product="small subunit ribosomal RNA"
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BASE COUNT
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 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 985 GCCTCAATAAAGACACACACCGATCCC 957

RESULT 10
 YSASRSUH/c 1723 bp rRNA linear PLN 12-FEB-2001
 LOCUS C.vismwanathii small subunit ribosomal RNA.
 DEFINITION M60309
 ACCESSION M60309.1 GI:176368
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Candida viswanathii
 Candida viswanathii
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; mitosporic Saccharomycetales; Candida.
 1 (bases 1 to 1723)
 Barns, S.M., Lane, D.J., Sogin, M.L., Bibeau, C. and Weisburg, W.G.
 Evolutionary relationships among pathogenic Candida species and
 relatives
 J. Bacteriol. 173 (7), 2250-2255 (1991)
 JOURNAL 91177814
 MEDLINE 2007550
 PUBMED
 FEATURES Location/Qualifiers

source 1. 1723
 /organism="Candida viswanathii"
 /mol_type="rRNA"
 /db_xref="taxon:5486"
 /tissue_11b="ATCC 22891"
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BASE COUNT
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 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1052 GCCTCAATAAAGACACACACCGATCCC 1024

RESULT 11
 YSASRSUG/c 1736 bp rRNA linear PLN 12-FEB-2001
 LOCUS C.tropicalis small subunit ribosomal RNA.
 DEFINITION M60308
 ACCESSION M60308.1 GI:176367
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Candida tropicalis
 Candida tropicalis
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; mitosporic Saccharomycetales; Candida.
 1 (bases 1 to 1736)
 Barns, S.M., Lane, D.J., Sogin, M.L., Bibeau, C. and Weisburg, W.G.
 Evolutionary relationships among pathogenic Candida species and
 relatives
 J. Bacteriol. 173 (7), 2250-2255 (1991)
 JOURNAL 91177814
 MEDLINE 2007550
 PUBMED

FEATURES Location/Qualifiers
 1. 1736
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 /mol_type="rRNA"
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BASE COUNT
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 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1051 GCCTCAATAAAGACACACACCGATCCC 1023

RESULT 12
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 LOCUS C.parapsilosis small subunit ribosomal RNA.
 DEFINITION M60307
 ACCESSION M60307.1 GI:176366
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Candida parapsilosis
 Candida parapsilosis
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; mitosporic Saccharomycetales; Candida.
 1 (bases 1 to 1739)
 Barns, S.M., Lane, D.J., Sogin, M.L., Bibeau, C. and Weisburg, W.G.
 Evolutionary relationships among pathogenic Candida species and
 relatives
 J. Bacteriol. 173 (7), 2250-2255 (1991)
 JOURNAL

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MEDLINE      91177814
PUBMED      2007550
FEATURES
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Location/Qualifiers
1. 1739
/organism="Candida parapsilosis"
/mol_type="rRNA"
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1. 1739
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Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

rRNA
1 GCGTCATTAAGAAACAACACCGATCCC 29
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Db      1054 GCGTCATTAAGAAACAACACCGATCCC 1026

RESULT 13
AB013533/1 1766 bp DNA linear PLN 11-DEC-1999
LOCUS      AB013533
DEFINITION Candida lodderae 18S rRNA gene, strain JCM 1601, partial sequence.
ACCESSION  AB013533
VERSION     AB013533.1 GI:4586721
KEYWORDS
SOURCE
ORGANISM
Candida viswanathii
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE
1 (sites)
Sugita,T. and Nakase,T.
Non-universal usage of the leucine CUG codon and the molecular
phylogeny of the genus Candida
Syst. Appl. Microbiol. 22 (1), 79-86 (1999)
JOURNAL
MEDLINE
PUBMED
10188281
2 (bases 1 to 1766)
Sugita,T.
Direct Submission
Submitted (30-APR-1998) Takashi Sugita, The Institute of Physical
and Chemical Research (RIKEN), Japan Collection of Microorganisms
(JCM); 2-1 Hirosawa, Wako, Saitama 351-0198, Japan
(E-mail:sugita@pharm.ac.jp, Tel:81-48-462-1111(ex.5135),
Fax:81-48-462-4619)
FEATURES
SOURCE
Location/Qualifiers
1. 1766
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Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

rRNA
1 GCGTCATTAAGAAACAACACCGATCCC 29
|||||
Db      1032 GCGTCATTAAGAAACAACACCGATCCC 1004

RESULT 14
AB013549/1 1767 bp DNA linear PLN 11-DEC-1999
LOCUS      AB013549
DEFINITION Candida sojae 18S rRNA gene, strain JCM 1644, partial sequence.
ACCESSION  AB013549

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VERSION      AB013549.1 GI:4586737
KEYWORDS
SOURCE
ORGANISM
Candida sojae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE
1 (sites)
Sugita,T. and Nakase,T.
Non-universal usage of the leucine CUG codon and the molecular
phylogeny of the genus Candida
Syst. Appl. Microbiol. 22 (1), 79-86 (1999)
JOURNAL
MEDLINE
PUBMED
10188281
2 (bases 1 to 1767)
Sugita,T.
Direct Submission
Submitted (30-APR-1998) Takashi Sugita, The Institute of Physical
and Chemical Research (RIKEN), Japan Collection of Microorganisms
(JCM); 2-1 Hirosawa, Wako, Saitama 351-0198, Japan
(E-mail:sugita@pharm.ac.jp, Tel:81-48-462-1111(ex.5135),
Fax:81-48-462-4619)
FEATURES
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Location/Qualifiers
1. 1767
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/mol_type="genomic DNA"
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/db_xref="taxon:52253"
<1. 1767
/product="18S ribosomal RNA"
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Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

rRNA
1 GCGTCATTAAGAAACAACACCGATCCC 29
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Db      1033 GCGTCATTAAGAAACAACACCGATCCC 1005

RESULT 15
AB013589/1 1768 bp DNA linear PLN 11-DEC-1999
LOCUS      AB013589
DEFINITION Candida viswanathii 18S rRNA gene, strain JCM 9567, partial
sequence.
ACCESSION  AB013589
VERSION     AB013589.1 GI:4586777
KEYWORDS
SOURCE
ORGANISM
Candida viswanathii
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE
1 (sites)
Sugita,T. and Nakase,T.
Non-universal usage of the leucine CUG codon and the molecular
phylogeny of the genus Candida
Syst. Appl. Microbiol. 22 (1), 79-86 (1999)
JOURNAL
MEDLINE
PUBMED
10188281
2 (bases 1 to 1768)
Sugita,T.
Direct Submission
Submitted (30-APR-1998) Takashi Sugita, The Institute of Physical
and Chemical Research (RIKEN), Japan Collection of Microorganisms
(JCM); 2-1 Hirosawa, Wako, Saitama 351-0198, Japan
(E-mail:sugita@pharm.ac.jp, Tel:81-48-462-1111(ex.5135),
Fax:81-48-462-4619)
FEATURES
SOURCE
Location/Qualifiers
1. 1768
/organism="Candida viswanathii"
/mol_type="genomic DNA"
/strain="JCM 9567"

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Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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